Copyright

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB DB
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-947-965-76
US-08-952-991A-32535
US-08-9514-302-4
US-09-514-302-2
US-09-514-302-2
US-09-152-060-64
US-09-152-060-64
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US-09-233-352-6
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US-08-471-044-29
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                                sequence
71, Appl
37535, Appl
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RESULT 2
US-09-252-991A-32535
; Sequence 32535, Applic
; Sequence 32535, Applic
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MARC J.
; TITLE OF INVENTION:

Application US/09252991A

Rubenfield et al.
NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

Query Matches Best Local Matches 1 Qy 1 Db 13 Qy 7 Db 18	US-08-947-965 Sequence 71 Patent No. (GENERAL INF GENERAL INF GAPPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT ITITLE OF IN FILE REFERR CURRENT PIL EARLIER APPLEARLIER FIL EARLIER APPLEARLIER A	p.	44440000000000000000000000000000000000
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12.3%; Score 77.5 imilarity 24.0%; Pred. No.; Conservative 22; Mismatc; FAKHPWFQIEDNRCYIDNGKLFARGSIVGNI	ion US/08947965A in, Lubbert Bauke Carsten aus von der Cyclomaltodextrin Gluc Variants 204-US NUMBER: US/08/947,965A 1997-10-09 NUMBER: 0477/95 1995-04-21 1995-04-21 1995-10-17 NUMBER: 113/95 1995-11-16 NUMBER: PCT/DK96/00179 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22 1996-04-22	ALIG	9 2 US-088 9 2 US-088 9 2 US-088 9 2 US-088 9 3 US-099 9 4 US-099
12.3%; Score 77.5; DB 3; Leng imilarity 24.0%; Pred. No. 0.67; Conservative 22; Mismatches 44; Ind TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGG	Glucanotransferase ,965A 00179	AL I GNMENTS	471-046A-32 470-566B-29 470-566B-32 838-219B-2 469-334-29 3469-334-29 3469-334-29 300-529-32 300-529-32 333-336A-2 233-356A-2 233-752A-2 233-752A-2 402-036-2 402-036-2 402-036-2 402-036-2 402-036-2
12.3%; Score 77.5; DB 3; Length 676; imilarity 24.0%; Pred. No. 0.67; Conservative 22; Mismatches 44; Indels 13; Gaps 3 EACHPWFQIEDURCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP 71			Sequence 32, Appl Sequence 29, Appl Sequence 32, Appl Sequence 4, Appli Sequence 29, Appl Sequence 29, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 6, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32535
LENGTH: 729
RESULT 4
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; TYPE: PRT
; ORGANIEM: Bacillus ohbensis
US-08-947-965-76
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CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 0477/95
EARLIER FILING DATE: 1995-04-21
EARLIER APPLICATION NUMBER: 1173/95
EARLIER APPLICATION NUMBER: 1281/95
EARLIER FILING DATE: 1995-10-17
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1995-11-16
EARLIER FILING DATE: 1995-04-22
EARLIER FILING DATE: 1996-04-22
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Best Local Similarity 29.3
Matches 34; Conservative
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Patent No. 6004790
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijketra, Bauke
APPLICANT: Andersen, Carsten
APPLICANT: Osten, Claus von der
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 4285.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                  12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP 71
                                                                                                                                          72 GE-SLKWNVRNLDVMPIFETLALRLVLQGDVIWL-RCVPELRVD 113
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                                                                                                                                                                                                                                                                                                        Similarity
                                                                                              YEDSIYRNLYDLADYDLNNTVMDQYLKESIKLWLDKGIDGIRVD 222
                                                                                                                                                                                   TPNHSSPALETDPSYAENGAVYNDGVLIGNYSN---DP-----NNLFHHNGGTDFSS 178
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29.3%; Pred. No. 2.3;
ative 16; Mismatches
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25.0%; Pred. No. 4.8;
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    VDLARVRERLRRLAVELLKAGDVVLLRC 659

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CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: 08/952,084
EARLIER FILING DATE: 1997-11-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. SEQ ID NO 2
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Best Local
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APPLICANT: IGARASHI,
APPLICANT: OZAKI, Ka
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENE FOR ENZYME HAVING TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE FILE REFERENCE: 2173-105P CURRENT APPLICATION NUMBER: US/09/514,302 CURRENT FILING DATE: 2000-02-28 EARLIER APPLICATION NUMBER: 08/952,084
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APPLICANT: ITO, Susumu
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NUMBER OF SEQ ID NOS: 14
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APPLICANT: OZAKI, Katsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ITO, Susumu
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tent No. 6338959
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                                                                                                                                                                                                                                                                                 LENGTH: 1938
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                                                        1127 SVKSGWKLIDEMYAY--DGKLGAELHEDGTATLKÝWSPKADNVSVVLÝDKÝDQNEVÝ--D 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
66 DVEFVPGESLKWNVR 80 : | | | : | : |
                                                                                              12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDFKAD-----YGGVGENLYVHAD 65
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                                                                                                                                                             Similarity
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                                                                                                                                          Conservative
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                                                                                                                                          11.0%; Score 69; DB 32.0%; Pred. No. 31; bive 11; Mismatches
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SEQ ID NO 100
LENGTH: 240
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                                                                                   EARLIER APPLICATION NUMBER: 60/068,368 EARLIER FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                            SOFTWARE: PatentIn Ver.
                                                              NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/US98/04858
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLICANT: Rosen et al.
TLE OF INVENTION: 28 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 LDKSQLPSLGNLKENFRTLGFDPGHDYSIPYLWGTTG----YSYDTAKVPGGRLEESWK 443
                                                                                                                                                                                              APPLICATION NUMBER: 60/048,189
FILING DATE: 1997-05-30
APPLICATION NUMBER: 60/057,765
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o. 6448230
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                                                                                                                                                       APPLICATION NUMBER: 60/048,970
                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,357
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LENGTH: 335
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                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (297)
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (35) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring
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64482
203 ELYVVVDNAEFOMLGSEAAVRHRVLEVVNHVDKLYQKLNFRVVLVGLEIW 252
                                                                    151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/068,368
                                60 -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
                                                                                                       14 KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN---
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APPLICATION NUMBER: 60/050,934
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29; Conserv
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RESULT 10
US-09-430-702-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-706-216-6
GENERAL INFORMATION:
APPLICANT: SCHULZ, GEORG E.
APPLICANT: PARSIEGLA, GOSTZ
APPLICANT: CANDUSSIO, AUTON
APPLICANT: WICH, GUNTER
TITLE OF INVENTION: CYCLODEXTRIN GLYCOSYL TRANSFERASES FOR PRODUCING
TITLE OF INVENTION: Y-CYCLODEXTRIN
FILE REFERENCE: SCHULZ-W2 CIP
CURRENT APPLICATION NUMBER: US/09/430,702
CURRENT FILING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: 09/816,317
                                                                                                                                                                                                                                       Sequence 1, Application US/09430702
Patent No. 6472192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DXTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP----GDSLPSRETRYV 202
                                                                                                                                                                                                                                                                                                                                                                                                                60 -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN------
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                                                                                                                                                                                                                                                                                                                                                                        ELYVVVDNAEFOMLGSEAAVRHRVLEVVNHVDKLYQKLNFRVVLVGLEIW 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 67; DB 3; Length 391; 26.4%; Pred. No. 6.2;
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                                                 US-08-960-780-4
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08960780
                                                                                                                                                                                              TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bacillus sp. 1-1
                                                                                                                                                                                                                                           NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: MA-708 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide OF INVENTION: Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Gainesville
                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 30-OCT-1997
                                                               INDIVIDUAL ISOLATE: 36a
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF 69
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                              790 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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Dullum, Charles Joseph
Muller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stockhoff, Brian A. Schmeits, James
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                                                                                                                linear
                                                                                                                                                                                                                                352-375-8100
                                                                                             protein
                                                                                                                               single
 10.5%;
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25.9%; Pred. No. 1.1;
cive 10; Mismatches
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 Score
Pred.
 No.
   DB 3;
21;
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REGISTRATION NUMBER: 39,355 REFERENCE/DOCKET NUMBER: MA-708C1 TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100 INFORMATION: 4: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 790 amino acids TYPE: amino acid STRANDEDNESS: single TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein RIGHNAL SOUNCE: INDIVIDUAL ISOLATE: 36a US-09-073-898-4	EADABLE YPE: PI G SYSTEM FI G SYSTEM FI G SYSTEM FI CATION FI CATI	RESULT 12 US-09-073-898-4 ; Sequence 4, Application US/09073898 ; Patent No. 6242669 ; Patent No. 6242669 ; GENERAL INFORMATION: APPLICANT: Feitelson, Jerald S. APPLICANT: Schmepf, H. Ernest APPLICANT: Schmeits, James APPLICANT: Loewer, David APPLICANT: Dullum, Charles Joseph APPLICANT: Stamp, Lisa APPLICANT: Muller-Cohn, Judy APPLICANT: Morill, George APPLICANT: Morill, George APPLICANT: Finstad-Lee, Stacey ITILE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleot ITILE OF INVENTION: Sequences Which Encode These Toxins NUMBER OF SEQUENCES: 144 ; CORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 ; CTTY: Gainesville COUNTRY: US	Matches 32; Conservative 13; Mismatches 32; Indels 60; Gaps Qy 3 EDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADY
		Nucleotide	60; Gaps 8

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APPLICANT: Daworski, Jan G.
APPLICANT: POSt-Beittenmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FAFTY ACID ELONGASES
FILE REFERENCE: 07148/064001
CURRENT APPLICATION NUMBER: US/08/868,373
CURRENT FILLING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 516
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-08-868-373-14
                                                                                                 ORGANISM: Acinetobacter baumannii US-09-328-352-8096
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US-09-328-352-8096
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US-08-868-373-14
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                                                                                                                                      Sequence 8096, Application US/09328352

Patent No. 6562258

Patent No. 6562258

GENERAL IMPORMATION:
APPLICANT: Gary L. Beton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNMERE: US/09/328,352

CURRENT APPLICATION UNMERE: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8096

LENGTH: 587

TYPE: PRT
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Best Local S
Matches 32
Query Match 10.3%; Score 65; DB 4; Length 587; Best Local Similarity 23.9%; Pred. No. 19; Matches 21; Conservative 21; Mismatches 38; Indels
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Best Local Similarity
Matches 21; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 --GVYLILKSQNGDEAW 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 RFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLD--VMPI-----FETLALRL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 10.5%; Score 66; DB 3; Length 790; Il Similarity 23.4%; Pred. No. 21; 32; Conservative 13; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 VLQGDV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 TLALRIVIQ---GDVIW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 -----EFVPGESLKWNVRNLDVMPIFE 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 65.5; Dinilarity 31.8%; Pred. No. 14; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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RESULT 15
US-09-252-991A-17381
; Sequence 17381, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; Patent No. 6551795
; GENERAL INFORMATION: ROUGHEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17381
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17381
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Search completed: January 22, 2004, 11:38:42 Job time: 22.7747 secs
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                                                                                                      193 QQKPD 197
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                                                                                                                                                          109 ELRVD 113
                                                                                                                                                                                                             138 TÉVYPGVVDTLKMLKRNGVEMALITNKPERFVAPILDEMKLGRYFRWIIGGDTL----P 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 PGESLKWNVRNLDVMPIFETLALRLVLQ 98
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                                                                                                                                                                                                                                                              67 VEFVPG--ESLKWNVRN------LDVMPIFETLAL----RLVLQGDVIWLRCVP 108
                                                                                                                                                                                                                                                                                                                    87 İEKVRQWİGNGARVLVRRALAĞSI------EHDĞİĞEEETEAALALFMEAYADSHAL 137
                                                                                                                                                                                                                                                                                                                                                            20 IEDNRCYIDNG-KLFARGSIVGNMSRFVFDPKADYGGVGEN-----LYVHADD--- 66
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2 6/ptcdata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptcdata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2 6/ptcdata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptcdata/2/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptcdata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptcdata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptcdata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptcdata/2/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptcdata/2/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptcdata/2/pubpaa/US08 NEW PUBCOMB.pep:*
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629
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/ cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 3 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
629 91 75.5 69 67.5 67.5 67.5 67.5 67.5	Score
100.0 14.5 12.0 11.0 11.0 10.8 10.7 10.7 10.7 10.7 10.7 10.7	Query Match
199 186 301 893 1938 444 444 6291 6291 240 2240 335	Length DB
115 115 114 114 112 112 112 112 112 112	!
US-10-300-393-19 US-10-300-393-20 US-10-369-493-2939 US-10-014-436-4 US-10-014-436-2 US-10-369-493-7954 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-10-375-932-89 US-09-853-161-64 US-09-853-161-64 US-09-853-161-64	ID
Sequence 19, Appl sequence 20, Appl Sequence 4, Appli Sequence 2, Appli Sequence 7954, Appli Sequence 25, Appli Sequence 25, Appli Sequence 89, Appl Sequence 88, Appl Sequence 41, Appl Sequence 100, App Sequence 100, App Sequence 100, App Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl	Description

45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
63	63	63.5	64	64	64	64	64	64	64	64	64	65	65	65.5	65.5	65.5	65.5	65.5	66	66.5	66.5	66.5	66.5	٥.		67	67	67	67
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φ	11	12	12	12	10	5	5	15	15	15	12	12	12		12	12	12	12	10	12	12	12	12	12	12	15	12	12	10
US-09-827-040-10	US-09-557-796-30	US-10-369-493-10822		-10-452-002A-	0-351A-	-10-099-285-9	US-10-099-285-94	US-10-099-285-92	-10-099-285-	US-10-099-285-78	US-10-369-493-18267	US-10-369-493-8159	US-10-137-113-36	US-09-883-797-14	US-10-375-932-97	375-932-9	-10-	US-10-375-932-26	5	US-10-120-801-18	369	US-10-369-493-12480	-10-375	US-10-375-932-38	L04-047-	US-10-226-844-1	211-884-	-10-210-951-5	US-09-852-797-64
\vdash	Sequence 30, Appl		Sequence 45, Appl			96,	94,	92,	80,	78,	182	819	e 36, Ap	14,	97	90,	Sequence 33, Appl	26,	4	Sequence 18, Appl	221	1248		38,	3709	Sequence 1, Appli	Sequence 58, Appl	e 58,	e 64,

ALIGNMENTS

RESULT 1 US-10-300-393-19

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RESULT 2
US-10-300-393-20
; Sequence 20, Application US/10300393
; Publication No. US20030118568A1
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Publication No. US20030118568A1
GENERAL INFORMATION:
APPLICANT: Crew, Mark D.
TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection TITLE OF INVENTION: Xenografts
FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18 —
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 629; DB 15; Best Local Similarity 100.0%; Pred. No. 2.6e-68; Matches 116; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 199
                                                                                                                                 28 AGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL
                                                                                                                                                                                                                                                      1 AGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL 60
                                                                                                                                                                                                                                                                                                                                                           Length 199;
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                                                                                                                                                                                                                                                                                                                      0;
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APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2939
LENGTH: 301
TYPE: PRT
ORGANISM: Thermotoga maritima
US-10-369-493-2939
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; ORGANISM: human cytomegalovirus Towne strain US3
US-10-300-393-20
                                                                                            US-10-014-436-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-369-493-2939
                   Sequence 4, Application US/10014436 Publication No. US20020182699A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Local Similarity
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PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 22
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TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection TITLE OF INVENTION: Xenografts
FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
APPLICANT: HATADA, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                        263 -APEELIKDLLKNWNVSNIVIRKPNLEDVFLKL 294
                                                                                                                                                                                                                                                                                                                                 19 QIEDNRCYIDNGKLFARG-----SIVGNMSRFVFDFKAD----YGGVGENLYVHADDVE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 RGAYFEWNIGGHPVPHTVDMVDI--TLSTR---WGDPKKYAACVPQVRMDYSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 FRVEENQCWSHMGMLHYKGRMSGNFTEKHFVSVGIVSQSYMDRLQVSGEQYHHDE----
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                                                                                                                                                                                                                                                                                     RLSDHVCIIDHGKIIAEGTPSSLISSSGLKTVVEFDCDQDVNVRYLEKKENHYVVETD--
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 75.5; DB 32.3%; Pred. No. 0.96;
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27.4%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
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0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
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                                                                                        US-10-014-436-2
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 111547/1995
PRIOR FILING DATE: 1995-05-10
PRIOR PRILING DATE: 1996-05-10
PRIOR PILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: US 09/514,302
PRIOR APPLICATION NUMBER: US 09/514,302
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
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Best Local Similarity 32.0%;
Matches 24; Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10014436 Publication No. US20020182699A1
Query Match
Best Local Similarity
                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Gene for Enzyme Having Both Alkaline Pullulanase and Alkaline Alp?
TITLE OF INVENTION: Amylase Activites
FILE REFERENCE: 2173-01229
CURRENT APPLICATION NUMBER: US/10/014,436
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: UT 111547/1995
PRIOR PILING DATE: 1995-05-10
PRIOR FILING DATE: 1995-05-10
PRIOR FILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR PILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR PILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
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PRIOR APPLICATION NUMBER: US 08/952,084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
TITLE OF INVENTION: Gene for Enzyme Having
TITLE OF INVENTION: Amylase Activites
FILE REFERENCE: 2173-0122P
CURRENT PEPLICATION NUMBER: US/10/014,436
CURRENT FILING DATE: 2002-05-21
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                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                              ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 893
TYPE: PRT
                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 DVEFVPGESLKWNVR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 SVKSGWKLIDEMYAY--DGKLGAELHEDGTATLKVWSPKADNVSVVLYDKVDQNEVV--D 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD-----YGGVGENLYVHAD 65
                                                                                                                                                                                 1938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARA, Katsutoshi
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11.0%;
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Pred. No. 23;
11; Mismatches
   Score
Pred.
   No.
      DB 14;
59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Both Alkaline Pullulanase and Alkaline Alph
                                 Length 1938;
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25.0%;

Pred. No. 15;

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US-10-375-932-25; Sequence 25, Application US/10375932; Publication No. US20040009469A1
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; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7954
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7954
LENGTH: 384
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                                                                                                                  NUMBER OF SEQ ID NOS: 345
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 448
TYPE: PRT
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Best Local Similarity
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Query Match
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                                                                                                                                                                                                               FILE REFERENCE: 0322.210US
CURRENT APPLICATION NUMBER: US/10/375,932
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/360,030
PRIOR FILING DATE: 2002-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Punnonen, Juha
APPLICANT: Brinkman, Alice M.
TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
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                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                          OTHER INFORMATION: Synthetic polypeptide: 16B4-NPRM
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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    10.7%; Score 67.5;
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  DB 12;
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  Length 448;
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; Sequence 89, Application US/10375932
; Publication No. US20040009469A1
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US-10-369-493-585
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                                                     NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 585
LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 585, Application US/10369493 Publication No. US20030233675A1
ORGANISM: Deinococcus radiodurans -10-369-493-585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Apt, Doris
APPLICANT: Punnonen, Juha
APPLICANT: Brinkman, Alice M.
TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
FILE REFERENCE: 0322.210US
                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/360,030
PRIOR FILING DATE: 2002-02-26
                                                                                                                     CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 GEDA-----PCKIP-FSTEDEKGVTQNGRLITANPIVTEKDSPVNIEAEPPFGESYIVV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 GEDA-----PCKIP-FSTEDEKGVTQNGRLITANPIVTEKDSPVNIBAEPPFGESYIVV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 GVGDKAL---
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                                                                                                                                                                                                                                                                        Hinkle, Gregory J.Slater, Steven C.Goldman, Barry S.Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                          Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 67.5; D
25.0%; Pred. No. 15;
Live 12; Mismatches
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NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 6291
TYPE: PRT
ORGANISM: Streptomyces refuineus
US-10-329-079-41
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                                                                                                      CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILLING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILLING DATE: 1998-09-11
PRIOR FILLING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILLING DATE: 1998-03-12
PRIOR FILLING DATE: 1998-03-14
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILLING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                  Sequence 100, Application US/09853161
Patent No. US20020076756A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
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Publication No. US20030198981A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED
FILE REFERENCE: 3002-11US
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CURRENT FILING DATE: 2002-12-24
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                       APPLICATION NUMBER: 60/050,934 FILING DATE: 1997-05-30
                                                            APPLICATION NUMBER: 60/040,710 FILING DATE: 1997-03-14
APPLICATION NUMBER: 60/048,100
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Pred. No. 20;
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    JS-09-852-659A-100
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SEQ ID NO 100
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LENGTH: 240
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CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
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TITLE OF INVENTION: 28 Human Secreted Proteins
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PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
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PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
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TYPE: PRT
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                                                                                                                SOFTWARE: PatentIn
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APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
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Pred. No. 7.8;
LB; Mismatches 35; Indels
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GENERAL INFORMATION:

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RESULT 14
US-09-853-161-64
; Sequence 64, Application US/09853161
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-100
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Best Local (
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Best Local Similarity
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FITLE OF INVENTION: 28 Human Secreted Proteins
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Patent No. US20020077287A1
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SEQ ID NO 64
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                                                                                                                                                                         GENERAL INFORMATION:
                                                CURRENT APPLICATION NUMBER: US/09/852,659A CURRENT FILING DATE: 2001-05-11 PRIOR APPLICATION NUMBER: 60/265,583 PRIOR FILING DATE: 2001-02-02
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NAME/KEY: SITE
LOCATION: (35)

OTHER INPOMMATION: X

NAME/KEY: SITE
LOCATION: (297)
                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
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TITLE OF INVENTION: 28 Human Secreted Proteins
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NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 335
TYPE: PRT
OTHER: INFORMATION: Xaa equals any of the naturally occurring L-amino acids FEATURE:
NAME/KEY: SITE
LOCATION: (35)
OTHER: INFORMATION: Xaa equals any of the naturally occurring L-amino acids FEATURE:
NAME/KEY: SITE
LOCATION: (297)
OTHER: INFORMATION: Xaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-659A-64
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Watches 29; Conserve
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PRIOR APPLICATION NUMBER: 60/068,368
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APPLICATION NUMBER: 60/048,189
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ADDITION NUMBER: 60/048,189
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FILING DATE: 1997-09-05
151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV 202
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Search completed: January 22, 2004, 12:09:28 Job time: 283.676 secs 밁 Ś В

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

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ALIGNMENTS

A; Molecule type: DNA A; Residues: (1-199) < WES> A; Residues: (1-199) < WES> A; Cross-references: EMBL: X04650; NID: 959801; PIDN: CAB37096.1; PID: 94456177 A; Cross-references: EMBL: X04650; NID: 959801; PIDN: CAB37096.1; PID: 94456177 A; Experimental source: strain AD169 A; Experimental source: strain AD169 R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Brown, C.M.; Cerny, R.; Horsnell, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Brown, C.M.; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R; Chee, M.S.; Brown, C.M.; Chee, M.S.; Brown, C.M.; Chee, M.S.; Bankier, A.T.; Brown, C.M.; Chee, M.S.; Brown, C.M.; Chee, M C;Genetics: A;Gene: HQLF2 C;Superfamily: cytomegalovirus HQLF2 protein C;Keywords: glycoprotein; transmembrane protein C;Keywords: glycoprotein; transmembrane for the file of A;Molecule type: DNA A;Residues (1-199-CHE) A;Residues (1-199-CHE) A;Cross-references: RWBL:X17403; NID:g59591; PIDN:CAA35313.1; PID:g1780933 A;Experimental source: strain AD169 A;Note: this sequence was submitted to the EMBL Data Library, December 1989 R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; l. M.; Barrell, B.G. Curr. Top. Microbiol. Immunol. 154, 125-169, (1990) A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09749; MUID:90269039; PMID:2161319 A;Recession: S09916 A;Status: nucleic acid sequence not shown, translation not shown HQLF2 protein precursor - human cytomegalovirus (strain AD169) N;Alternate names: hypothetical protein US2 C;Species_human_cytomegalovirus, human herpesvirus 5 C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000 C;Accession: E26078; S09916 Ş 밁 8 R; Weston, K.; Barrell, B.G. J. Mol. 192, 177-208 1986 A;Title: Sequence of the short unique region, short repeats, and A;Reference number: A92935; MUID:87169717; PMID:3031311 A;Accession: E26078 밁 RESULT 1 Matches Query Match Local 116; 88 61 28 ۲ Similarity AGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL YVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDYTS 143 YVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDYTS 116 AGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL Conservative 100.0%; Score 629; DB 1; 100.0%; Pred. No. 5.8e-58; tive 0; Mismatches 0; Length 199; Indels 0, part of the long repeats Gaps 87 60 0

T.; F

RESULT QQBEC6

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A;Experimental source: strain AD169
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cern
M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09917
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                               probable N-acetylmuramoyl-L-alanine amidase (imported) - Yersinia pestis (strain C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: glycoprotein; transmembrane protein
F;11-5/Domain: signal sequence #status predicted <SIG>
F;26-186/Product: hypothetical protein US3 #status predicted <MAT>
F;160-182/Domain: transmembrane #status predicted <TMM>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Note: this sequence was submitted to
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A;Experimental source: strain AD169
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A; Residues: 1-186 <WES>
                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-254 <KUR>
                                                                                                                                                                                                                                                             A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                                                                            A;Accession: AD0205
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Best Local 9
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                                         Matches
                                                            Query Match
Best Local (
                                                                                                                                                           Cross-references: GB:AL590842; PIDN:CAC90504.1;
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PWKS---TAKHPWFQIEDNRCYIDN--GKLFARGSIVGNMSRFVFDPKADYGGVGENLYV
                                         Conservative
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27.0%;
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Pred. No. 0.01;
4; Mismatches
                                                          Pred.
                                                          Score 78.5;
Pred. No. 1.
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                                         Mismatches
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                                         Gaps
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A;Reference name of compared with conceptual translation
A;Accession: S26399
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-703 <SCH>
A;Residues: 1-703 <SCH>
A;Residues: 30-52 <SC2>
C;Function:
C;Function:
A;Description: catalyzes the breaking and reformation of 1,4-alpha-D-glucopyranosyl bonds
A;Note: can also catalyze the disproportionation transfer of 6 to 8 1,4-alpha-D-glucopyra
C;Superfamily: cyclomaltodextrin glucanotransferase; alpha-amylase core homology
C;Keywords: calcium; duplication; extracellular protein; glycosyltransferase; hexosyltran
F;1-29/Domain: signal sequence #status predicted <SIG>
F;1-29/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: scyclomaltodextrin glucanotransferase #status experimental <MAT>
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T21532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyclomaltodextrin glucanotransferase (EC 2.4.1.19) precursor - Bacillus sp. N;Alternate names: cyclodextrin glycosyltransferase C;Species: Bacillus sp. C;Bate: 31-Mar-1993 #Bequence_revision 31-Mar-1993 #text_change 24-Apr-1998 C;Accession: S26399; S26593 R;Schmid, G.; Englbrecht, A.; Schmid, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A;Reference number: Z19435
A;Accession: T21532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein P28H7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Berks,
                                                                                                           F;30-703/Product: cycloma
F;30-160/Domain: A1 <DA1>
F;161-224/Domain: B <DOB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: אלסיסיי הערכה (C;Accession: אלסיסיי האלסייים (C;Accession: אלסיסיים האלסייים האל
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                       F;429-516/Domain:
                                                       F;219-353/Domain: alpha-amylase
F;225-428/Domain: A2 <DA2>
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429-516/Domain: C <DOC>
517-600/Domain: D <DOD>
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                                                                                 core homology <AMY:
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Pred. No. 2.
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, N.; Linia, M.; Shinagawa, H. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A98629; MUID:21156231; PMID:11258796
A;Accession: A98950
                                                                                                                                                                                                                                                                                                hypothetical protein ECs2569 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: A99950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;52,54,57,58,76,78/Binding site: calcium (Asp, Asn, Asn, Gly, A F;68-75/Disulfide bonds: #status predicted F;161,212,221,255/Binding site: calcium (Asn, Ile, Asp, His) #status F;251,279,350/Active site: Asp, Glu, Asp #status predicted
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                                                              A;Cross-references: GB:BA000007; PIDN:BAB35992.1; PID:g13362037; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                         A; Molecule type: DNA
A; Residues: 1-261 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001718; GB:AE000512; NID:g4980881; PIDN:AAD35474.1; PID:g49808:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-301 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3C transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
  Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEDSIYRNLYDLADYDLNNTVMDQYLKESIKFWLDKGIDGIRVD
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conserved hypothetical protein HI0360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 75.5; 32.3%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 301;
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on, D.;
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C;Superf
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Matches 13
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                 Query Match
Best Local
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C;Accession: C64948
R;Blattner, F.R.; Plunkett
A.; Rose, D.J.; Mau, B.;
                                                                                                                                                                                             F;11-27/Domain: transmembrane #status predicted <TM1>
F;38-54/Domain: transmembrane #status predicted <TM2>
F;58-74/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000280; GB:U00096; NID:g1788163; PIDN:AAC74929.1; PID:g1788166; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64948
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A;Cross-references: GB:AE005174; NID:g12515915; PIDN:AAG56849.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Perna, N.T.; Plunkett III, G.; Burland, iller, L.; Grotbeck, E.J.; Davis, N.W.; L. Nature 409, 529-533, 2001
                                                                                       F;213-229/Domain:
F;240-256/Domain:
                                                                                                                                                                                                                                                                C; Superfamily: conserved hypothetical protein HI0360 C; Keywords: transmembrane protein; transport protein
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-261 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein yebI - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E85798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                    ;127-143/Domain: transmembrane
                                                                                                                                 182-198/Domain:
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  1 Similarity
13; Conserv
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13; Conserv
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ilarity 40.6%;
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                                                                                       transmembrane
transmembrane
                                                                                                                                   transmembrane
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Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t III, G.; Burland, V.; Mau, B.; Glasner, J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%;
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                                                                                                               #status
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Score 74; DB
Pred. No. 3.8;
8; Mismatches
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Pred. No. 3.8;
8; Mismatches 1
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Pred. No. 3.8;
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                                                                                          ~TM6 > 
~TM7 > 
~TM8 >
                                           Length 261;
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A; Map position: cir
C; Superfamily: Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AGR C_4118 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: F97631
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C; Superfamily: S
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AI2854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A; Residues: 1-360 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-360 <KUR>
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Best Local (
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Best Local (
                                                                                                                                                                                              Superfamily: Synechocystis hypothetical protein slr1087
                                                                                                                                                                                                                                                                                              Cross-references: GB:AE007869; PIDN:AAK88007.1; PID:g15157422; GSPDB:GN00169
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17; Conservative
                                                                                                   . Similarity 17; Conserv
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                                                KSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDFKADYGGVGENLYVHADDVEF 69
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                                                                                                                       11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 74; DB 26.6%; Pred. No. 5.5; tive 12; Mismatches
                                                                                                                         Score 74; DB 2; Length 360; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller, N.; Blanchard, M.; Qurollo, B.; Gold. Doughty, D.; Scott, C.; Lappas, C.; Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -IDNIESLAFGPVVD----GKQIFVIASDDNF
  IDNIESLAFGPVVD----
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kelz, B.;
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                                                                                      A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-391,1375-1409 <MIL>
A;Residues: 1-391,1375-1409 <MIL>
A;Residues: 1-391,1375-1409 <MIL>
A;Residues: 1-391,1375-1409 <MIL>
B;YOSHIOka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, TeMBO J. 9, 535-541, 1990
B;MBO J. 9, 535-541, 1990
A;Title: Virus-11ke particle formation of Drosophila copia through auto A;Reference number: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835; MUID:90151630; PMID:1689241
                                                                                                                                                                                                                                                                                                                                                                                  A;Actession type: DNA
A;Molecule type: DNA
A;Residues: 1-1409 <MOU>
A;Cross-references: GB:M11240; NID:g158615; PIDN:AAA74497.1;
A;Cross-references: GB:M11240; NID:g158615; POOO, A.O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PH1933 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E71208
                                                                                                                                                                                                                                                                                            R;Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
Nucleic Acids Res. 17, 2134, 1989
A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA
A;Reference number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612;
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1207
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 5, 1630-1638, 1985
A;Title: Complete nucleotide sequence of the Drosophila transposable element copia: homol
A;Reference number: A03324; MUID:85267679; PMID:2410772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic A;Molecule type: DNA
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C;Accession: A03324; S03612; S14835
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C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-159 < KAW>
                      A;Cross-references: EMBL:X54147; NID:g7749; PIDN:CAA38086.1;
                                                  A;Residues: 1-391,1375-1409 <YOS>
                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A03324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Mount, S.M.; Rubin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia
N;Contains: copia protein, 31K; copia protein, 48K; proteinase
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Best Local Similarity
Matches 22; Conserv
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Pred. No. 3;
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                              PID: 97750
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A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
                                                                                                        ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2963
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                           A; Molecule type: DNA
A; Residues: 1-394 < KUR>
                                                                                                                                                                                                           Science 294, 2317-23
A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                          R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin,
                                                                                                                                                                                                                                                                                                                                                                                                phosphomannose isomerase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable siderophore biosysnthesis protein YPO0778 [imported] - Yersinia pestis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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A;Cross-references: GB:AE008689; PIDN:AAL44124.1; PID:g17741695; GSPDB:GN00187
                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-2201 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: AB0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Yersinia pestis
Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001;
Accession: AH0095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;2-433/Product: copia protein, 48K #status predicted <MAT1>;2-270/Product: copia protein, 31K #status predicted <MAT2>;271-433/Product: proteinase #status predicted <MAT3>
                                                                                                                                                                                                                                                                                                                                                                  Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:AL590842; PIDN:CAC89627.1; PID:g15978856; GSPDB:GN00175;
                                                                                                                                                                                                                                                                                                                                            Accession: AF2963
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Best Local (
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                                                                                                                                                                                                                                         P.; Romero, P.; Zhang, S.
294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDMTRMNNFKRYLMEKFRMTDLNEIKHFIGIRIEMQEDKIYL 1137
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28.2%; Pred. No.
                                                                                                                                                                                                           Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%; Score 72;
23.5%; Pred. No.
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A;Gene: Atu3311
A;Map position: linear chromosome
                                                                                                                                                                                                        A;Experimental source: strain C58 C;Genetics:
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134 QAAASLPERKDEMRVRALDILAILE 158
                           65 DDVEFVPGESLKWNVRNLDVMPIFE 89
                                                         82 PWKDALSHGLSWFE----KVYRLENG---LYGNLADQTGRLI-DPSFDLYNQAFALFAAA 133
                                                                                                                    23;
                                                                                      8 PWKSTAKH--PWFQIEDNRCY-IDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHA 64
                                                                                                                    Conservative
                                                                                                                                  11.2%;
27.1%;
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                                                                                                                                  Score 70.5;
Pred. No. 1;
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Search completed: January 22, 2004, 11:42:39 Job time: 23.3788 secs

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Result
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Maximum Match 100%
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/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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G/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
G/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
G/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
G/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
G/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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             5 US-10-300-393-19
4 US-10-300-393-29
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4 US-10-029-009-34
1 US-09-766-378A-36
1 US-09-927-122-3
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1 US-09-927-128-3
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1 US-09-927-120-3
1 US-10-084-298-10
2 US-10-084-298-10
1 US-09-847-208-26
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Sequence 3, A
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Sequence 24, I
Sequence 10, A
Sequence 10, A
Sequence 26, A
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Sequence 20, Appl
Sequence 20, Appl
Sequence 325, Appl
Sequence 325, App
Sequence 34, Appl
Sequence 36, Appl
Sequence 3, Appli
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Sequence 29, Appli
Sequence 21, Appli
Sequence 26, Appli
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US-10-131-409-83	-150-811-		US-09-925-299-923	US-09-925-299-923	-017-754-	US-10-113-872-340	-274-375-		-09-849	US-09-902-941-340	9-736-457-	-10-120-	US-10-104-047-3709	US-10-014-436-2	-10-014-436-	US-10-329-079-41	-10-410-842A-6	US-10-410-842A-56	0-133-973-	US-10-029-009-12	US-10-410-842A-2	US-10-369-300-13	US-10-410-842A-6	US-10-410-842A-30	US-10-410-842A-44	US-10-410-842A-40	-10-264-	64-634-2	US-10-152-190-6
83,	85,	85,	9	923,	340	340	Sequence 3, Appli	34(Sequence 340, App	e 340,	340,	e 18	Sequence 3709, Ap	2	4	41	69	56	74,	12	e 2,	13	6	e 30,	e 44,	e 40,	Sequence 39, Appl	23,	Sequence 6, Appli

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; TYPE: PRT
; ORGANISM: human cytomegalovirus Towne strain US2
US-10-300-393-19
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                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 19
                                                                                                                                                                                                                                        Matches 136;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection
TITLE OF INVENTION: Xenografts
FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 22
140
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                                                                                                                                                                              RLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD 81
                       DYTSSAYMWNMQYGMV 157
                                                                                                  YGGVGENLYVHADDVEFVÞGESLKWNVRNLDVMÞIFETLALRLVLQGDVIWLRCVÞELRV 141
DYTSSAYMWNMQYGMV 155
                                                                                                                                                           RLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD
                                                                             YGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRV 139
                                                                                                                                                                                                                                  78.1%; Score 740; DB 15; illarity 100.0%; Pred. No. 1.5e-77; Conservative 0; Mismatches 0;
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US-10-029-009-20
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Publication No. US20030118568A1
GENERAL INFORMATION:
APPLICANT: Crew, Mark D.
APPLICANT: Crew, Mark D.
TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection of TITLE OF INVENTION: Wenografts
FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT APPLICATION NUMBER: US 60/342,981
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 186
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Best Local Similarity
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APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR PILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: human cytomegalovirus Towne strain US3
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                                                                                                                       10 VFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVG
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                                                                                   4 VLVLAILAVLFLRLADSVPRPLDVVV----SEIRSAHFRVEENQCWSHMGMLHYKGRMSG
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NFTEKHFVSVGIVSQSYMDRLQVSGEQYHHDE----
                                          NMSR-----RVFDPKADYGGVGENLYVHADDVEFVPGESLKWNV-----RNLDVMPI 116
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No. US20020164617A1
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                                                                                                                                                                                           12.1%; Score 115; DB 15; 24.1%; Pred. No. 4.9e-05;
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-RGAYFEWNIGGHPVPHTVDMVDI
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US-10-029-009-22
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Felsch, Jason S.
APPLICANT: Annis, David Allen
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 498
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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Nash, Huw M.
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                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10044692
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51.8%;
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Pred. No. 0.00071;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-044-539-325; Sequence 325, Approximation No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                   Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 RAPRCRAVRSLLRSHYREVLPLATFV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 EDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVFMVVYISYIYARLPDGITKAG--EDA-----LRPWKSTAKHPWFQI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 11.6%; Score 109.5; DB Similarity 32.1%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTORCVLLRTWEALAPATPAMP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
CLASSIFICATION:
                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10044539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDARPPPAAPSFRQVSCLKELVARVLQRLC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1189;
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                                                                                                                                                                                                                                                                                                                                                                                                             DIAGNOSTIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                         US-10-029-009-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                   TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins FILE REFERENCE: 111025.173 US2 CURRENT APPLICATION NUMBER: US/10/029,009 CURRENT FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: US 60/258,970 PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Felsch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Kalghaegi, Krishna
APPLICANT: Nash, Huw M.
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-03.
INFORMATION FOR SEQ ID NO: 325:
                                                              OTHER INFORMATION: Met-Melitin SS-FLAG M1 tag-m2 mAchR sequence
                                                                                       FEATURE:
                                                                                                                              TYPE: PRT
                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                     ENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-OCT-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 RAPRCRAVRSLLRSHYREVLPLATEV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKFLVNVALVFMVVYISYIYARLPDGITKAG--EDA-----LRPWKSTAKHPWFQI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P----WDARPPPAAPSFRQVSCLKELVARVLORLC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/912,951 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10029009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1189 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US20020164617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 109.5; DB 32.1%; Pred. No. 0.0026;
11.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
  DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1189;
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Query Match

Matches

Best Local Similarity

<u>.</u>

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TOPOLOGY: linear;
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-766-378A-36
                                                                  US-09-927-122-3
                                                                                                                                           밁
                                                                                       RESULT 9
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              Sequence 3, Application US/09927122 Publication No. US20030012782A1 GENERAL INFORMATION:
                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                     Query Match
APPLICANT: GOLD,
                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: COTIESE, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 4800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSFECATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiao, Jin-an
Jiao, Jin-an
Jiao, Hing C.
Wong, Hing C.
WONG: SOLUBLE MHC COMPLEXES AND
METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKFLVNVALVFMVVYISYIYARLPD
                                                                                                                                                                                                               l Similarity
21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKFLVNVALVFMVVYISYIYADYKD 25
                                                                                                                                                                     MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/960,190 FILING DATE: 29-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
COUNTRY: usa
                                                                                                                                           MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09766378A
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                                                                                                                                                                                                                 Conservative
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Acevedo, Jorge
Burkhardt, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.0%; Pred. No. 0.0035;
                                                                                                                                                                                                              10.8%; Score 102; DB 9; 100.0%; Pred. No. 8.4e-05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48002-DIV
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                                                                                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                 Indels
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APPLICANT: GOLD, DANIEL P.
APPLICANT: SHOPES, ROBERT J.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR ALTERING A B
TITLE OF INVENTION: PATHOLOGY
TILE REFERENCE: 032077.0003
CURRENT APPLICATION NUMBER: US/09/927,121B
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3
LENGTH: 21
TYPE: PRT
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                                    US-10-361-849-8
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US-10-361-849-8
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10361849
Publication No. US20030170619A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09927121B Publication No. US20030082178A1 GENERAL INFORMATION:
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LENGTH: 21
TYPE: PRT
ORGANISM: Apis mellifera
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Best Local
                                                                                                 SEQ ID NO 8
LENGTH: 21
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TITLE OF INVENTION: METHOD AND COMPOSITION FOR ALTERING A T CELL MEDIATED TITLE OF INVENTION: PATHOLOGY FILE REFERENCE: 032077.0002 CURRENT APPLICATION NUMBER: US/09/927,122 CURRENT FILING DATE: 2001-08-10 NUMBER OF SEQ ID NOS: 58 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                     APPLICANT: Hara, Toshio
TITLE OF INVENTION: Nucleic Acid Capable of Promoting Gene Expression
FILE REFERENCE: 027847.00102US01
CURRENT APPLICATION NUMBER: US/10/361,849
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/355,752
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
                                                         TYPE: PRT
ORGANISM: Apis mellifera
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Length 21;
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Query Match

10.8%;

Score 102;

DB 12;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR APPLICATION STEP 2000-12-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
APPLICANT:
                                                            NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver.
SEQ ID NO 10
                                                                                                                                                                PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/256,977
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/10/084,298
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Composition and Method for Treating Inflammatory TITLE OF INVENTION: Disorders FILE REFERENCE: GI5358 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jacobs, Kenneth
APPLICANT: Pittman, Debra
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                                                                                                                           PRIOR FILING DATE: 2000-04-28
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                               APPLICATION NUMBER: 09/561,811
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Annis, David Allen
Kalghatgi, Krishna
Nash, Huw M.
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Fouser, Lynette
Spaulding, Vikki
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             APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 70
                                                                                                                                                                                                                                                                                      US-09-847-208-26
; Sequence 26, Application US/09847208
; Publication No. US20030082190A1
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RESULT 14
US-10-084-298-10
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                                                                                                                                                                    US-10-084-298-10
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
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Publication No.
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CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Composition and Method for Treating Inflammatory
TITLE OF INVENTION: Disorders
FILE REFERENCE: GI5358 CIP
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/561,811 PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/281,353
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                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Amino acid tag
                                                                                                                                                                                                                                                       LENGTH: 49
TYPE: PRT
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                                                               10.8%; Score 102; DB 15; Local Similarity 100.0%; Pred. No. 0.00026; les 21; Conservative 0; Mismatcher
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Fouser, Lynette
Spaulding, Vikki
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Maximum Match 100%
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Perfect score:
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68	68.5	68.5	68.5	69.5	69.5	69.5	70	70.5	71	71.5	72	76.5	76.5	77.5		80	82
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316	1384	640	130	521	472	358	448	327	405	1266	675	316	316	729	310	676	1938
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US-08-585-595-3	US-08-826-134-2	US-09-252-991A-27542	US-08-826-134-12	US-08-276-213-3	US-08-985-492-13	US-08-604-913B-11	US-09-724-623-84	US-09-107-532A-6181	US-09-252-991A-28582	US-08-506-296B-4	US-08-947-965-76	US-09-736-457-340	US-09-702-705-340	US-09-252-991A-32535	US-09-252-991A-17381	US-08-947-965-71	US-09-514-302-2
Sequence 3, Appli	Sequence 2, Appli	Sequence 27542, A	Sequence 12, Appl	Sequence 3, Appli	Sequence 13, Appl	Sequence 11, Appl	Sequence 84, Appl	Sequence 6181, Ap	Sequence 28582, A	Sequence 4, Appli	Sequence 76, Appl	Sequence 340, App	Sequence 340, App	Sequence 32535, A	Sequence 17381, A	Sequence 71, Appl	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-08-974-549A-613 Sequence 6: Patent No. COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: US 08/844,419 GENERAL INFORMATION: FILING DATE: 18-APR-19
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US
FILING DATE: 25-APR-19
PRIOR APPLICATION DATA: APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR APPLICATION DATA:
APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: APPLICANT: NUMBER OF SEQUENCES: APPLICATION NUMBER: FILING DATE: 06-MAY ZIP: 94111-3834 COUNTRY: ADDRESSEE: APPLICATION NUMBER: 613, Application US/08974549A San Francisco California E: Townsend and Two Embarcadero Lingner, Joachim UMBER: US 08/851,843 06-MAY-1997 09-MAY-1997 25-APR-1997 18-APR-1997 Thomas R US 08/911,312 US 08/846,017 US 08/854,050 US 08/912,951 Townsend and Crew LLP Center, Eighth Floor Version Catalytic Subunit #1.30

FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 08/915,503

FILING DATE: 14-AUG-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 325, Application US/08912951
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
                                                                                                                                                                                                          APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                        CITY: San Francisco
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                                                              COUNTRY:
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LOCATION: 1..1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 RAPRCRAVRSLLRSHYREVLPLATEV----RRLGPOGWRLVORGDPAAFRALVAQCLVCV 115
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                                                                                  Californ:
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                                                                                                                                                                                                                                                                                          Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                              United States of
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melittin signal sequence and full length
hTRT protein"
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                                                                   America
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                                                                                                                                                                                                                                    DIAGNOSTIC AND
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                                                                                                                                                                                              US-08-960-190A-36
                                                                                                                                                          Sequence 36, Appli
Patent No. 6232445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                      GENERAL INFORMATION:
APPLICANT: Rhode,
APPLICANT: Aceved
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                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
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PRIOR APPLICATION NUMBER: U
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APPLICATION NUMBER: US 0
FILING DATE: 09-MAY-1997
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CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
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               TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
                                                    APPLICANT:
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CLASSIFICATION:
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CLASSIFICATION: 435
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                          116 P----WDARPPPAAPSFRQVSCLKELVARVLQRLC 146
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                                                                                                                                                                                                                                                                                                                                              60 RAPRCRAVRSLLRSHYREVLPLATFV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                50 EDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF------V
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                                                                                                                                                                               Application US/08960190A
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             Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
WENTION: SOLUBLE MHC COMPLEXES AND
VENTION: METHODS OF USE THEREOF
                                                                                                                            Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                       Jorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 109.5; DB 4; 32.1%; Pred. No. 0.00063; zive 10; Mismatches 65;
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CORRESPONDENCE ADDRESS:

Bronstein, Roberts & Cushman, LLP

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US-09-376-330-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.
APPLICANT: Thomas, David Y.
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                     Matches
                                                                                                  Best Local Similarity
                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGGT
FILE REFERENCE: 2139-9"US"
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 199-08-18
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 21 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTLESS, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 4800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                               LENGTH: 21
TYPE: PRT
ORGANISM: Melittin Signal Peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-CCT-1997
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
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                                                                 Conservative
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                                                                                               Score 102; DB 4;
Pred. No. 1.2e-05;
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; Pred. No. 1.2e-05;
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                                                                                                                                   Length 21;
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RESULT 6
US-08-793-958-2
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                                                                                                                                                                                                           Sequence 2,
Patent No. 5
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APPLICANT: Cohen, (
APPLICANT: Bisenbe:
APPLICANT: Nicola,
                                                                                                                                                                                                                                                                                                                                                                            Matches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cohen, Gar
APPLICANT: Eisenberg,
APPLICANT: Nicola, An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: No. 5654174 and, Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                            CORRESPONDENCE ADDRESS:
                                                                                            NUMBER OF SEQUENCES:
                                                                                                             APPLICANT: Nicola, Anthony IITLE OF INVENTION: Herpes IITLE OF INVENTION: Variant
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                              STREET:
                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                           159 QPELAPEDPEDSALLEDPV 177
             Chicago
Illinois
                                                                                                                                                                                                                          Application US/08793958
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                                                                                                                                                                                                                                                                                                            QPELAPEDPEDSALLEDPV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive
                                              6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bisenberg,
USA
                                                                                                                                                                          Cohen, Gary H.
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                Marshall,
                                                                                                                                                                                                                                                                                                                                                                                           10.5%;
                                                                                                               Herpes Simplex Virus Glycoprotein Variants
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                                                                                                                                                           Roselyn J.
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                                              O'Toole, Gerstein, Murray & Borun
ower, 233 S. Wacker Drive
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Pred. No
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COMPUTER READABLE FORM:

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US-08-139-609-1
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Best Local Similarity
Matches 19; Conserv
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Patent No. 5837249
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
APPLICANT: Dietzschold, Bernhare
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5814486and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,946
PILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/685,459
PILING DATE: 12-APR-1991
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 antino acids
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,609
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/047,443
FILING DATE: 08-MAY-1987
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TITLE OF INVENTION: Method for Generating an
TITLE OF INVENTION: Cell Response Protective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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STREET: Spring House Corporate Cntr., P.O. Box
CITY: Spring House
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Against a Virus
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RESULT 8
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TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
D NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5470718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:5:
LENGTH: 383
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cohen, Ga:
APPLICANT: Eisenberg
APPLICANT: Nicola, AI
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                           Sequence 11, Application US/08499568 Patent No. 5654174
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                        STREET: 5..
CITY: Chicago
STATE: Illinois
STATE: USA
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APPLICATION NUMBER: US/07/954,417
FILING DATE: 30-SEP-1992
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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LENGTH: 369 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 19-APR-1985 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 10.5%; Score 99; Local Similarity 100.0%; Pred. No. hes 19; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 561,553
FILING DATE: 01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                                                                                                      159 QPELAPEDPEDSALLEDPV 177
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    Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive

                                                                                                                                                                                                       Bisenberg, Roselyn J.
Nicola, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%; Score 99; DB 6; ilarity 100.0%; Pred. No. 0.0021; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                            Cohen, Gary H.
                                                                                                                                                                      Herpes Simplex Virus Glycoprotein D
Variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11:
                                                                                       NAME: No. 5814486and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,958
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Roselyn J.
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes Simpl
TITLE OF INVENTION: Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NO. 5654174 and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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TELEX: 25-3856
                                                         TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No
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5814486
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6300 Sears Tower, 233 S. Wacker Drive
388 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes Simplex Virus Glycoprotein D
Variants
15
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US-08-220-151-23
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                                                                                                                          US-08-220-151-23
                                                          Query Match
Best Local S
Matches 19
                                                                                                                                                                                                           TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                       MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/220,151 FILING DATE: 30-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                              TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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70. 5529780
289
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                     159 QPELAPEDPEDSALLEDPV 177
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                                                           l Similarity
19; Conserv
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                                                                                                                                                                                                     amino acid
OPELAPEDPEDSALLEDPV 307
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                                                        10.5%; Score 99; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                   linear
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NUCLEOTIDE AND AMINO ACID SEQUENCES OF
CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris & Safford
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                                                             Mismatches
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5. 0.0022;
0;
                                                           DB 1; Le
. 0.0022;
ches 0;
                                                                                        Length 393;
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RESULT 12 US-08-413-118-23

Sequence 23, Application US/08413118
Patent No. 5688920
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO

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RESULT 13
US-08-473-446-23
                                                                                                                              equence equence action:
GENERAL INFORMATION:
APPLICANT: LIMBACH, KEITH J.
APPLICANT: LIMBACH, KEITH J.
APPLICANT: LIMBACH, KUCLEOTIDE AND AMINO ACID SEQUENCES OF TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-413-118-23
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 QPELAPEDPEDSALLEDPV 177
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530 FIFTH AVENUE,
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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N-terminal
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100.0%; Pred. No. 0.0
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORRIS & SAFFORD, P.C.
AVENUE, 25TH FLOOR
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US/08/473,446
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. 0.0022;
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5182195-10
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US-08-499-568-4
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LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5182195

APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIHIKO;YOSHIMURA, 1

TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE

DEFICIENT YEASTS
                                                                                                                                                                                                                                        Sequence 4, Application US/08499568 Patent No. 5654174
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Best Local Similarity
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                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                         APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Rosely
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes S
TITLE OF INVENTION: Variante
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 71
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
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LENGTH: 393 amino acids
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TELEFAX: (212) 840-0712
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
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                                             STATE:
                                                                            STREET:
                  ZIP: 60606
                          COUNTRY:
                                                                                           ADDRESSEE:
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                                             Chicago
: Illinois
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100.0%; Pr/
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                                                                                                                                            Herpes Simplex Virus Glycoprotein Variants
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100.0%; Pred. No. 0.
tive 0; Mismatches
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                                                                            O'Toole,
Tower, 233
                                                                                                                                                                                           Roselyn J
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S. Wacker Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,568
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 564174and, Greta E.
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 38813
TELCOMMUNICATION UNDERS: 35,302
REFERENCE/DOCKET NUMBER: 38813
TELECHMUNICATION UNDERS: 35,302
REFERENCE/DOCKET NUMBER: 38813
TELECHMUNICATION UNDORMATION:
TELEPHONE: (312) 474-0448
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: protein
US-08-499-568-4

Query Match
Query Match
10.5%; Score 99; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Oy
20 QPELAPEDPEDSALLEDPY 177
Db 290 QPELAPEDPEDSALLEDPY 177
Db 290 QPELAPEDPEDSALLEDPY 177
Db 290 QPELAPEDPEDSALLEDPY 308
Search completed: January 22, 2004, 11:38:43
Job time : 34.2253 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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   seq length: 0
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B 8	Дb	· VQ	유 성	Query Ma Best Loo Matches	A;Gene: HQLF2 C;Superfamily C;Keywords: g F;1-25/Domain F;26-199/Prod F;161-186/Dom F;68/Binding	A; Note: thi	A;Cross	A;Statu	A;Title A;Refero A;Acceso	M.; Bar; Curr. To	A; Exper: R; Chee,	A; Resido A; Cross	A; Kerero A; Acceso A; Moleco	A;Title	R;Weston	C;Date:	N;Alteri	RESULT :	٠	443 543
142 DY:		82 YG	22 RLI 20 RLI	atch cal Simi 136;	HQLF2 family: cy rds: glyco Domain: si 9/Product: 86/Domain: nding site	this sequice:	A; Residues: 1-199 (Chb) A; Cross-references: EMB; A; Experimental source:	A;Status: nucleic ac A;Molecule type: DNA	A; Title: Analysis of A; Reference number: A; Accession: S09916	M.; Barrell, B.G. Curr. Top. Microbiol.	A;Experimental source: strain AD169 R;Chee, M.S.; Bankier, A.T.; Beck,	A; Residues: 1-199 < WES> A; Cross-references: EMB	A; Reference number: A; Accession: E26078 A; Molecule type: DNA	Sequence:	n, K.; Bai	C;Date: 30-Sep-1989 #sequent C:Accession: E26078: S09916	ngura process procured summas cycomegy N,Alternate names: hypothetical protein C:Species: human cytomegalovirus human	rotein pre		73.5 73.5 73
DYTSSAYMWNMQYGMV 157	SVGENLYV	GENLYV	PDGITKAG PDGITKAG	78. ilarity 100 Conservative	/tomegal pprotein lgnal se hypoth transm	ience wa	BS: EMBL	DNA	of the er: S097	oiol. Im	ource: s nkier, A) <wes></wes>)78 DNA	of the	crell, B)78: S09	s: hypot			7.8 7.8 7.7
MOYGM	HADDV	HADDV	EDALR	78.1%; 100.0%; ative	oviru tra quenc etica embra hydra	s sub	:X174	equen	prot	muno1	train	:X046	3	shor		uence	hetic	·		557 757 463
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5 7	YGGVGENLYVHADDVEFVPGESLKWNVRNLDVWPIFETLALRLVLQGDVIWLRCVPELRV	YGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRV	RLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDDKAD	Score 740; DB 1; Pred. No. 1.1e-64); Mismatches 0	A;Gene: HQLF2 C;Superfamily: cytomegalovirus HQLF2 protein C;Superfamily: cytomegalovirus HQLF2 protein C;Keywords: glycoprotein; transmembrane protein C;Keywords: signal sequence #status predicted <sig> F;1-25/Domain: signal sequence #status predicted <mat> F;26-199/Product: hypothetical protein US2 #status predicted <mat> F;161-186/Domain: transmembrane #status predicted <tmm> F;68/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmm></mat></mat></sig>	A; Note: this sequence was submitted to the EMBL Data Library,	A;Residues: 1-137 Curb? A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35313.1; A:Experimental source: strain AD169	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA. **Recidence 1.100 DNA. **Recidence 1.100 DNA.	A; Title: Analysis of the protein-coding content of the sequence A; Reference number: S09749; MUID: 90269039; PMID: 2161319 A; Accession: S09916	M.; Barrell, B.G. Curr. Top. Microbiol. Immunol. 154, 125-169, 1990	69 , S.; Bohni, R.; Brown,	A;Residues: 1-199 <wes> A;Residues: 1-199 <wes></wes></wes>	8/169/1/; PMID:303131	<pre>h. moi. biol. 192, 1/7-200, 1900 A,Title: Sequence of the short unique region, short repeats, h.mofercome number. 102025. With 07160717. DMTh.2021211</pre>		ision 30-Sep-1989 #te	nguis process procursor summan cycomegasorisms (octain motor) N;Alternate names: hypothetical protein US2 C.Snecies: human cytomegalovitus human hernesvitus S	vtomedalovitus (strai	ALIGNMENTS	T07909 B90572 D41853
	ALRIVLQGDVIWLRCVPELRV 139	ALRLVLQGDVIWLRCVPELRV 141	.FARGSIVGNMSRFVFDDKAD 81 FARGSIVGNMSRFVFDDKAD 79	Length 199; ; Indels 0; Gaps 0;	edicted <mat></mat>	library, December 1989	35313.1; PID:g1780933	not shown	s sequence of human cytomegalovirus 19	•	Ω .Σ	37096.1; PID:g4456177	1	peats, and part of the long repeats		C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000 C;Accession: R26078: S09916	201031	n AD169)		4-coumarate-CoA li lipoprotein [impor hexose phosphate t

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k; Weston, K.; Barrell, B.G.
J. Mol. Biol. 192, 177-208, 1986
A;Title: Sequence of the short unique region, short repeats, and A; Reference number: A92935; MUID:87169717; PMID:3031311
A; Accession: F26078
A; Molecule type: DNA
A; Residues: 1-107
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A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: $09749; MUID:90269039; PMID:2161319
A;Accession: $09917
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-186 <CHE>
A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35314.1; PID:g1780934
A;Experimental source: strain AD169
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:
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A;Gene: HQLF1
C;Superfamily: cytomegalovirus HQLF1 protein
C;Superfamily: cytomegalovirus HQLF1 protein
C;Koywords: glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-186/Product: hypothetical protein US3 #status predicted <MAT>
F;160-182/Domain: transmembrane #status predicted <TMM's
F;160-182/Domain: carbohydrate (Asn) (covalent) #status predicted
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C;Species: human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Accession: F26078; S09917
                                                                                                                                                                 N;Contains: melittin F
C;Species: Apis melifera (honeybee)
C;Species: Apis melifera (honeybee)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 15-Sep-2000
C;Accession: A91133; A91640; B61285; S23131; A01761; A18880
C;Accession: A91133; A91640; B61285; S23131; A01761; A18880
R;Vlasak, R.; Unger-Ullmann, C.; Kreil, G.; Frischauf, A.M.
Eur. J. Biochem. 135, 123-126, 138
Eur. J. Biochem. 135, 123-126, Coloned cDNA coding for honeybee prepromelity
A;Reference number: A91133; MUID:83287387; PMID:6309516
A;Cross-references: GB:X02007; NID:g5621; PIDN:CAA26038.1; PID:g5622
R;Habermann, E.; Jentsch, J.
Hoppe-Seyler's Z. Physiol. Chem. 348, 37-50, 1967
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A;Experimental source: strain AD169
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.;
M.; Barrell, B.G.
                                                                                      A; Molecule type: mRNA
A; Residues: 1-70 < VLA>
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Pred. No. 8.9e-05;
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A,Title: Isolation and structure of N(alpha)-formyl melittin.
A,Title: Isolation and structure of N(alpha)-formyl melittin.
A,Reference number: A91267, MUID:72098669; PMID:5139483
A,Reference number: A91267, MUID:72098669; PMID:5139483
A,Sontents: annotation; synthesis
A,Note: N-formyl-melittin major was isolated from the venom and its structure was confirm
R;Mollay, C.; Vilas, U.; Kreil, G.
Proc. Natl. Acad. Sci. U.S.A. 79, 2260-2263, 1982
A,Title: Cleavage of honeybee prepromelittin by an endoprotease from rat liver microsomes
A,Reference number: A18880; MUID:82247982; PMID:7048315
A,Contents: annotation; intact signal sequence after cleavage by partially purified signs
R;Eisenberg, D.; Gribskov, M.; Terwilliger, T.C.
submitted to the Brookhaven Protein Data Bank, October 1990
A,Reference number: A50496; pDB:2MIT
A,Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 44-69
R;Terwilliger, T.C.; Eisenberg, D.
J. Biol. Chem. 257, 6010-6015, 1982
A,Title: The structure of melittin. I. Structure determination and partial refinement.
A,Reference number: A30639; MUID:82189958; PMID:7076661
A,Reference number: A30639; MUID:82189958; PMID:7076661
A,Reference number: A30639; MUID:82189958; PMID:7076661
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A;Note: the structure of melittin was confirmed by synthesis of a
R;Kreil G; Kreil-Kiss, G.
Biochem. Biophys. Res. Commun. 27, 275-280, 1967
A;Title: The isolation of N-formylglycine from a polypeptide prese
A;Reference number: A90165; MUID:67248282; PMID:6040373
A;Reference number: A90165; MUID:67248282; PMID:6040373
A;Rontents: annotation
A;Note: about 10% of melittin is formylated at the amino end
A;Note: about 10% of melittin is formylated at the amino end
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A;Molecule type: protein
A;Residues: 44-69 <RAM>
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Blochem. J. 284, 663-665, 1992
A;Title: Effect of permethylation on the haemolytic activity of melittin.
A;Reference number: S23131; MUID:92321983; PMID:1622387
A;Accession: S23131
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A;Reference number: A91640; MUID:68327913; PMID:5592400
                                                                                                                                                                                                                                                                                                                                                                        F;1-21/Domain: signal sequence #status experimental <SIG>
F;22-43/Domain: propeptide #status experimental <PRO>
F;22-43/Domain: propeptide #status experimental <PRO>
F;44-69/Product: melittin major #status experimental <MAJ>
F;51-69/Product: melittin F #status experimental <MELP>
F;44/Modified site: formylated amino end (Gly) (in mature form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status experimental continuous form) (partial) #status exp
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J. Biol. Chem. 257, 6016-6022, 1982
A;Title: The structure of melittin. II. Interpretation of the A;Reference number: A30640; MUID:82189559; PMID:7076662
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Experientia 27, 765-767, 1971
                                                                                                                                                                                                            Local
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MKFLVNVALVFMVVYISYIYA 21
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A;Cross references: GB:K02372
C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-393/Product: glycoprotein D #status predicted <GPD>
F;341-360/Domain: transmembrane #status predicted <TMN>
C;341-360/Domain: transmembrane #status predicted <TMN>
VGBE17
glycoprotein D precursor - h
C; Species: human herpesvirus
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A;Residues: 1-3,'A',5-70,'N',72-83,85-269,'R',271-282,'P',284-364,'R',366-394 <LAS>
A;Residues: 1-3,'A',5-70,'N',72-83,85-269,'R',271-282,'P',284-364,'R',366-394 <LAS>
A;Experimental source: strain Hzt
C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane protein
F;119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Title: DNA sequence analysis of the type-common glycoprotein-D genes o A;Reference number: A90945; MUID:84131549; PMID:6321120
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C;Species: human herpesvirus 1
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
C;Accession: A94268; B90945; A03729
R;Watson, R.J.; Weis, J.H.; Salstrom, J.S.; Enquist, L.W.
Science 218, 381-384, 1982
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G;Date: 31-Dec-1993 #text_change
G;Date: 31-Dec-1993 #text_change
G;Accession: A90945; A03729
R;Lasky, L.A.; Dowbenko, D.J.
DNA 3, 23-29, 1994
TNA 3, 23-29, 1994
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C;Species: human herpesvirus 1
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A; Residues: 1-393 < LAS>
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                          human herpesvirus
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copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia N;Contains: copia protein, 31K; copia protein, 48K; proteinase C;Species: Drosophila melanogaster C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 16-Jul-1999 C;Accession: A03324; S03612; S14835 R;Mount, S.M.; Rubin, G.M. Mol. Cell. Biol. 5, 1630-1638, 1985
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A;Title: Molecular and biological characterization of a herpes simplex virus type 1 (HSV-A;Reference number: A47627; MUID:90324869; PMID:2165127
A;Accession: A47627
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C;Keywords: glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-394/Product: glycoprotein D #status predicted <GPD>F;342-358/Domain: transmembrane #status predicted <TMN>F;119,146,287/Binding site: carbohydrate (Asn) (covalent) #status
A;Molecule type: DNA
A;Residues: 1-1409 <MOU>
A;Cross-references: GB:M11240; NID:g158615; PIDN:AAA74497.1;
R;Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
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A; Residues: 1-394 <IZU>
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A; Residues: 1-394 < MCG>
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A;Title: Sequence determination and genetic content of the A;Reference number: A00656; MUID:85160822; PMID:2984429
A;Accession: A03730
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jun-2000
                                                                                                                   A; Reference number: A03324; A; Accession: A03324
                                                                                                                                                  A;Title: Complete nucleotide sequence of the A;Reference number: A03324; MUID:85267679; PA
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19; Conservative 0;
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100.0%; Pred. No. 0.
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PMID:2410772
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glycoprotein D precursor - h
C;Species: human herpesvirus
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A;Cross-references: FlyBase:FBgn0000349
A;Mobile element: retrotransposon copia
A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
C;Keywords: polyprotein; proteinase
C;Keywords: polyprotein; proteinase
F;2-433/Product: copia protein, 48K #status pr
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A;Molecule type: DNA
A;Moseidues: 1-391,1375-1409 <YOS>
A;Cross-references: EMBL:X54147; NID:g7749; PIDN:CAA38086.1; PID:g7750
C;Genetics:
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A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A;Reference number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612
                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:K02373; NID:g330270; PIDN:AAA45842.1; PID:g330271
C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
F;119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predic
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DNA 3, 23-29, 1984
A;Title: DNA sequence analysis of the type-common glycoprotein-D
A;Reference number: A90945; MUID:84131549; PMID:6321120
A;Accession: A03731
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C;Species: human herpesvirus 2
C;Date: 03-Aug-1984 #sequence_revision
C;Accession: A03731
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A;Title: Virus-like particle formation of Drosophila copia through autocatalytic process A;Reference number: S14835; MUID:90151630; PMID:1689241
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A; Residues: 1-393 <LAS>
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Matches 38; Conserv
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                                herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96.5; DB Pred. No. 0.63;
                                                                                                                                                                                                                                                        Score 91; DB 1
Pred. No. 0.46;
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                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-Aug-1984 #text_change
                                                                                                                                                                                                                                                                             DB 1;
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                                  (strain
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                                                                                                                                                                                                                                                                             Length 393;
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                                                                                                                   A;Molecule type: DNA
A;Residues: 1-313;314-787 <YOS>
A:Cross-references: DDBJ:D10880
                                                                                                                                                                                       Gene 120, 191-196, 1992
A;Title: Efficient amplification of Drosophila simulans
A;Reference number: PC1232; MUID:93013034; PMID:1383092
A;Accession: PC1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
             C;Superfamily: retrovirus-related
                                A;Cross-references: FlyBase:FBgn0012867
A;Mobile element: retrotransposon copia
                                                                              A;Gene: FlyBase:copia
                                                                                                 C;Genetics:
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RESULT 12
PC1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6 protein - human herpesvirus 2 (strain HG52)
C;Species: human herpesvirus 2
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: E43674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:K01408; NID:g330268; PIDN:AAA45841.1; C;Superfamily: herpesvirus glycoprotein D C;Keywords: glycoprotein; transmembrane protein C;Keywords: glycoprotein; transmembrane protein E;1-24/Domain: stgnal sequence #status predicted <SIG>F;25-393/Product: glycoprotein D #status predicted <GPD>F;340-356/Domain: transmembrane #status predicted <TMN>F;340-356/Domain: transmembrane 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-393 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 26, 307-312, 1983
A;Title: DNA sequence of the herpes simplex virus type 2
A;Reference number: A03732; MUID:84159516; PMID:6323270
A;Accession: A03732
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A03732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-393 <MCG>
A;Cross-references: EMBL:X04798
C;Superfamily: herpesvirus glycoprotein D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Watson,
                                                                              copia polyprotein - fruit fly (Drosophila simulans) retrotransposon copia (fragments) C;Species: Drosophila simulans C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: DNA sequence and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;MCGeoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C. J. Gen. Virol. 68, 19-38, 1987
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C;Accession: PC1232
R;Yoshioka, K.; Kanda, H.; Takamatsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A43674; MUID:87111457; PMID:3027242
A;Accession: E43674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                           QPELAPEDPEDSALLEDP 176
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Pred. No.
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N.; Togashi,

S.; Kondo,

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S.; Miyake, T.; Sakaki,

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RESULT 14
F75021
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A;Residues: 1-1578 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95868.1; PID:g16413076; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                               R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequen
A;Reference number: A75001
A;Accession: F75021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1512
              A; Experimental C; Genetics:
                                                   A;Molecule type: DNA
A;Residues: 1-159 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50612.1; PID:g545912
                                                                                                                                                                                                                                                                 ribosomal protein s18 alanine acetyltransf erase related protein PAB1226 - Pyrococcus C;Species: Pyrococcus abyssi C;Date: 20-Aug_1999 #sequence_revision 20-Aug_1999 #text_change 20-Jun-2000 C;Accession: F75021
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                                                                                                                               A;Status: preliminary
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C;Date: 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptidoglycan bound protein (LPXTG motif) adhesin homolog lin0636 [imported]
C;Species: Listeria innocua
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PAB1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 MVAVALVFQLVPWSNIFAGAEENQTKTTQQVTQPDNQKVADENKTTVIPDNKETTKNLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LVNVALVFMVVYISYIYARLPDGITKAGEDALRP--WKSTAKHPWFQIEDNR---CYIDN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKQLLKGSVDWNFTNKVTDAN---GNTKET-----YAPGDSLKFSL 110
                                        source: strain Orsay
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29.1%; Pred. No. 11;
tive 18; Mismatches
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RESULT 15
AD0205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Iil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, III. Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable N-acetylmuramoyl-L-alanine amidase [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0205
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                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-254 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: AD0205
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: AB0001;
                                                                                                                                                                                                                                                                                                                                                                     :Cross-references: GB:AL590842; PIDN:CAC90504.1; PID:g15979715; GSPDB:GN00175
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                                                                                                                                                                                                                                              33;
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                                      ETLALRIVI 126
                                                                              LCSLPSKNDIISKLKRYGYDTSGAVSEVGYNQLIRAFQLHFRP-
                                                                                                                                                             SNILYRFPD-ITPVNVVGHSDIAPGRKSDPGAAFPWKALYDAGIGAWYDDETKQRYLDQF 187
                                                                                                                                                                                                   SYIYARLPDGIT------KAGEDALRPWKS---TAKHPWFQIEDNRCYIDN- 58
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ETVAILYAL
                                                                                                                    -GKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIF 117
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                                                                                                                                                                                                                                              16; Mismatches
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947
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_organel:*
sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	ű	4	ω	N	L	Result No.
106.5	107.5	108.5	109.5	112.5	115	118	121	124	127	130	131	132	133	136	489	Score
11.2	11.4	11.5	11.6	11.9	12.1	12.5	12.8	13.1	13.4	13.7	13.8	13.9	14.0	14.4	51.6	Query Match
149	149	149	187	149	186	186	186	186	196	186	186	186	186	186	203	Length
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	DB.
Q918E7	Q918F1	Q910V7	Q8QRV4	Q918F4	Q8UZK6	Q910G4	Q918E9	Q918E2	Q8JKF7	Q918E6	Q918E4	Q910T7	Q918F0	Q918F3	Q8QRV5	ID
Q918e7 human cytom	Q918f1 human cytom	٠,	Q8qrv4 chimpanzee	Q918f4 human cytom	Q8uzk6 human cytom	Q910g4 human cytom	human	Q918e2 human cytom	Q8jkf7 cercopithec		Q918e4 human cytom	Q910t7 human cytom	Q918f0 human cytom		Q8qrv5 chimpanzee	Description

RESULT 2

45	44	43	42	41	40	39	38	37	36	ω 5	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
79	79	79	79.5	80	.80	80.5	80.5	80.5	82	83	84	84	•	84.5	85	91	91	96.5	97.5	99	99	99	99	99	99	99	100.5	101.5
8.3	8.3	8.3	8.4	8.4	8.4	æ .5	8.5	8 5	8.7	8 8	8.9	8.9	8.9	8.9	9.0	9.6	9.6	10.2	10.3	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.6	10.7
329	325	159	692	725	250	1582	415	404	1938	318	254	159	1578	1409	376	394	393	1017	149	394	394	394	394	394	394	394	149	149
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Q8N225	Q8UJM0	059596	030565	Q59239	Q8PBX2	Q8Y9A5	Q19894	Q8CVG5	P70983	Q93J07	Q8ZFL6	003060	Q92E25	Q08461	Q98FC4	9HNT6	Q69467	Q8T391	Q910D0	Q69082	Q8QRB6	Q05060	Q05059	Q69081	Q991M3	Q8QRB7	Q918E3	Q69186
Q8n225 homo sapien	Q8ujm0 agrobacteri	059596 pyrococcus	O30565 bacillus br	bacillus	Q8pbx2 xanthomonas	Q8y9a5 listeria mo	n	Q8cvg5 escherichia	P70983 bacillus sp	Q93j07 streptomyce			un	drosophila	4			Q8t391 drosophila	human	human	human	human	human	Q69081 human herpe	human	human	human	Q69186 human cytom

ALIGNMENTS

рь	P &	B 8	Quer Best Matc	SQ	DR :	몺	R	₽₽	RP.	R S	2 0	8	စ္တ	DE	DT.	DŢ	DI A	38	RESULT Q8QRV5
144 TSSAYMWNNOYGMV 157 : 146 TSNAYMWNNOYGMV 159	84 GVGENLYVHADDVEFVPGESLKMNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDY 143 	24 PDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYG 83 - - - - - - - - - - - -	Query Match 51.6%; Score 489; DB 12; Length 203; Best Local Similarity 63.4%; Pred. No. 6.2e-41; Matches 85; Conservative 24; Mismatches 23; Indels 2; Gaps 1;	SEQUENCE 203 AA; 23262 MW; CA131FD182BE8300 CRC64;		Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.	Alcendor D.J., Hayward G.S., McGeoch D.J.;	Davison A.J., Akter P., Dolan A., Wright K.M., Addison C.,	SEQUENCE FROM N.A.	[1]	Hetanerpesvirinae; Cytomegalovirus. NCBT TaxID=188763:			US2.	(TrEMBirel. 21, Last annotation	(TrEMBLrel, 21.	01-JUN-2002 (TremBirel. 21, Created)	Q8QRV5 PRELIMINARY; PRT; 203 AA.	LT 1 V5

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01-DEC-2001
01-DEC-2001
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                                                                                                                                          Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
"RL17, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413550; AAL14480.1; -.
SEQUENCE 186 AA; 21558 MW; 21D1DC5ADF43DD1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Betaherpesvirinae;
NCBI_TaxID=10359;
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                                                            VFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVG
                     NMSRFVFDPKADYGGVG-----ENLYV-----HADDVEFVPGESLKWNV-----RNL
                                             VLVLAILAVLFLRLADSVPR----PLNVVVSEIKSAHFRVEENOCWFHMGMLYFKGRMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                      DMVDI--TLSTR---WGDPKKYAACVPQVRMDYSSQTINWYLQRSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFT-----KKHFVNVGIVSQSYMDRLQVSGEQYHHDE----RGAYFEWNIGGYPVSHTV
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-KKHFVNVGIVSQSYMDRLQVSGEQYHHDE----RGAYFEWNIGGHPVTHTV
                                                                                                                                                                                                                                                              uses, no RNA stage;
Cytomegalovirus.
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26.5%;
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                                                                                        Score 133; UB - 1
Pred. No. 2.4e-05;
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Pred. No. 1.2e-
31; Mismatches
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rom the human cytomegalovirus
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RESULT 4

Q91077

ID Q910

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Viruses; dsDNA viruses, r
Betaherpesvirinae; Cytome
NCBI_TaxID=10359;
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Q910T7;
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"Characterization of transcripts from the human cytomegalovirus TRLT, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413649; AAL14477.1; -.
EMBL; AF413646; AAL14468.1; -.
EMBL; AF413647; AAL14471.1; -.
EMBL; AF413647; AAL14471.1; -.
EMBL; AF413647; AAL14471.1; -.
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Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
                                                                                       Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
"RL17, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF413663; AAL14519.1;
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Scott G.M., Barrell B.G., Oram
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Q8JKF7;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
SEQUENCE FROM N.A.
MEDLINE=22174937; PubMed=12186931;
Chang W.L., Tarantal A.F., Zhou S.S.,
"A recombinant rhesus cytomegalovirus
                                                                                                                                                                  Cercopithecine herpesvirus 8.
Viruses; dsDNA viruses, no RNA stac
Betaherpesvirinae; Cytomegalovirus
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"Characterization of transcripts from the human cytomegalovirus
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413657; AAL14501.1; -.
SEQUENCE 186 AA; 21679 MW; 7C0318DABA6E891D CRC64;
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Viruses; dsDNA viruses,
Betaherpesvirinae; Cytor
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Pred. No. 4.9e-05;
6; Mismatches 55
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  viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
[1]
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                                                                                                                                                                                                                                                Q918E9;
01-DEC-2001
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Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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J. Virol. 76:9493-9504(2002).
EMBL; AF474179; AAM97606.1; -.
SEQUENCE 196 AA; 23115 MW;
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01-DEC-2001
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Pred. No. 0.00
28; Mismatches
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"Characterization of transcripts from the human cytomegalovirus
TRLT, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413651; AAL14483.1; -.
SEQUENCE 186 AA; 21533 MW; CB68FEIE6BC76728 CRC64;
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STRAIN=27A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPĒCIES=Human cytomegalovirus; STRAIN=29A;
Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10363, 10359;
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Liu W., Zhao Y., Biegalke B.J.;
"Analysis of human cytomegalovirus US3 proteins.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                    FETLALRLVLQGD-VIWLRCVPELRVDYTSSAYMWNMQ 153
                                                                                                                                                                                                                                            VLVLAILAVLFLRLADSVPRPLDVVV----SEIRSAHFRVEENOCWFHMGMLHYKGRMSG
                                                                                                                                                                                                                                                                                         VFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVG
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                                  --TLSTR----WGDPKKYAACVPQVRMDYSSQTINWYLQ 147
                                                                                                                                       NFTEKHFVSVGIVSQSYMDRLQVSGEQYHHDE----RGAYFEWNIGGHPVPHTVDMVDI
                                                                                                                                                                                         NMSR-----FVFDPKADYGGVGENLYVHADDVEFVPGESLKWNV------RNLDVMPI
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Betaherpesvirinae; Cyto
                                                                                                                                     Scott G.M., Barrell B.G., Oram J., Rawlingon W.D.; "Charracterization of transcripts from the human cytomegalovirus TRL17, UL20a, UL36, UL65, UL94, US3 and US34."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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NMSRFVFDPKADYGGVG-----ENLYV-----HADDVEFVPGESLKWNV-
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Cytomegalovirus.
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01-DEC-2001
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Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;

Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;

"Characterization of transcripts from the human cytomegalovirus

TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF413649; AAL14478.1;

EMBL; AF413649; AAL14470.1;

EMBL; AF413647; AAL14472.1;

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Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=188763;
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01-JUN-2002 (TrEMBLrel. 21, Created)
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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12-JUN-2002 (TrEMBLrel. 21, Last sequence update)
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Pred. No. 0.0
Score 108.5; DB 12;
Pred. No. 0.0052;
3; Mismatches 49;
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"Characterization of transcripts from the human cytomegalovirus
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413650; AAL14481.1; -.
SEQUENCE 149 AA; 17201 MW; 0523494C741B3A79 CRC64;
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Cytomegalovirus.
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SUMMARIES
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P01593 methanococc
C50313 chlorobium
P071598 human immun
Q95586 pseudomonas
Q072m9 mus musculu
P17646 drosophila
Q06193 entamocba
P14090 haemophilus
Q06193 entamocba
P14090 haemophilus
Q08de8 rhizobium
P15635 rattus norv
P37679 escherichia
P13025 h rnal poly
P75473 mycoplasma
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유성

28

Query Match 100.0%; Score 629; DB 1; Best Local Similarity 100.0%; Pred. No. 3e-60; Matches 116; Conservative 0; Mismatches 0;

Length 199;

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Gaps

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87

AGEDALRPWKSTAKHPWPQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL

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	3; CAA353 6; CAB370 7; QOBEC5. 27-JUN-01 11 protein 68 172 188 172 188 199 AA;		GENOME. 026903; PubMe 026903; PubMe T., Hutchison T., Satchwell 05 the protect ovirus strain 0 Microbiol 0 Microbiol 0 Microbiol	FROM N.A. 7169717; p , Barrell of the sh ats of hum iol. 192:1	cytomegalovirus s; dsDNA viruses rpesvirinae; Cyt. axID=10360;	(Rel. (Rel. prote	STA		
200	CAA35313.1; CAB37096.1; QQBEC5. JUN-01. JUN-01; JUN-01; JUN-01 JU	y is instit inst inst inst licer licer	NOME. 80039; PubMed=216131 Bankier A.T., Beck S Bankier A.T., IECK Hutchison C.A. III Satchwell S.C., Tom if the protein-coding if the protein AD169."; Microbiol. Immunol. MITTY: BELONGS TO THE	775 0 8 6	rus uses Cyt	10, Created) 10, Last sequence 42, Last annotation HQLF2.	STANDARD;		378 380 435 458 462 517 718 997 1062 1375 1375
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820x2 630. DB 1.	cture. N-LINKED (GLCNAC N-LINKED (GLCNAC N-LINKED (GLCNAC 4DD2DF3D692393F3	t. It is production formatics tute. There as as long as it tremoved. Usament (See http:	9; Bohni R., Brow Kouzarides T., Inson P., Westor content of the g 154:125-169(1990) US2 FAMILY	Med=3031311; G.; t unique region, short repea cytomegalovirus.";	in AD169). RNA stage; Herpesviridae ılovirus.	ed) sequence update) annotation update)	PRT; 199 AA.	ALIGNMENTS	OPS4 DROME OPS4 DROME OPS4 DROPS PEPC LACLA ENGA HELPY ENGA HELPY ENGA HELPY Y11 HPV12 CDGT BACCI Y414 MYCPN CERU MOUSE RPOB VIBCH BLMH CHICK LP1G DROME
1000th 100.	.) (POTENTIAL)) (POTENTIAL)) (POTENTIAL). CRC64;	ed through a collaboration and the EMBL outstation - e no restrictions on its s content is in no way tge by and for commercial //www.isb-sib.ch/announce/	own C.M., Cerny R., Martignetti J.A., on K.M., Barrell B.G.; sequence of human	ats, and part of the	dae;				P08255 drosophila P29404 drosophila Q9ceg3 lactococcus Q25505 helicobacte Q92109 helicobacte Q92109 helicobacte P36733 human papil P30920 bacillus ci P75183 mycoplasma Q61147 mus musculu Q9kv30 vibrio chol P87362 gallus gall P811997 drosophila

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Best Local S
Matches 31
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01-MAR-1989
01-MAR-1989
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsmell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G., "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An enhancer element in the short unique region of human cytomegalovirus regulates the production of a group of abundant immediate early transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            weston K., Barrell B.G.;
"Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.";
J. Mol. Biol. 192:177-208(1986).
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                                                                                                                                                                                              Early protein;
CARBOHYD 6
                                                                                                                                                                                                            PIR; F26078; QQBEC6.
Early protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90269039; PubMed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 162:406-416(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88128558; PubMed=2829427;
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X04650; CAB37097.1; -.
M18921; AAA45958.1; -.
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                                                                                                                      31;
                                                                                                                                     Similarity
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                            FVPGESLKWNV-----RNLDVMPIFETLALRLVLQGD-VIWLRCVPELRVDYTS
                                                          FRVEENOCWFHMGMLYFKGRMSGNFTEKHF---VNVGIVSQSYMDRLQVSGEQYHHDE--
                                                                                       FQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL-----YVHADDVE
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186 AA;
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                                                                                                                                   Score 97; DB 1; Length 186; Pred. No. 0.0027;
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                                                                                                             ,.0027;
32;
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RESULT 3
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                                                                            Matches
                                                                                        Query Match
Best Local :
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Pfam; PF02806; alpha-amylase C; 1.
Pfam; PF00686; CBM 20; 1.
Pfam; PF01833; TIG; 1.
PRINTS; PRONTY
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P31746;
01-JUL-1993 (Rel. :
01-JUL-1993 (Rel. :
15-DEC-1998 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmid G., Englbrecht A., Schmid D.;

"Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase gene from the alkalophilic Bacillus 1-1.";

(In) Huber O., Szejtli J. (eds.);

Proceedings of the fourth international symposium on cyclodextrins, pp.71-76, Kluwer Academic Publishers, Dordrecht and Boston (1988).

-!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.

-!- COPACTOR: BINDS TWO CALCIUM IONS.
                                                                                                                                         DOMAIN
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CHAIN
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PRODOM; PD001568; CBD 4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; CBD 4.
InterPro; IPR006046; Glyco hydro_13.
InterPro; IPR002999; IPT_TIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UTL-1993 (Rel. 26, Created)
01-UTL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cyclomaltodextrin glucanotransferase precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S26399; ALBSX1.
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                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE LIN THE AMINO-TERMINAL SIDE CLEAVES THE ALEHA-1,4-GLUCOSIDIC BO. IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHE ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALFOOLIGOSACCHARIDE PRODUCED.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Monomer.
                          159
                                                 12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP
 72 GE-SLKWNVRNLDVMPIFETLALRLVLQGDVIWL-RCVPELRVD
                                                                                        Similarity
                        TPNHSSPALETNPNYVENGAIYDNGALLGN-----YSNDQQNLFHHNGGTDFSS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                 Glycosy]
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                                                                                                                                78663
                                                                            12.3%; Score 77.5; 1
24.0%; Pred. No. 1.5
tive 22; Mismatches
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BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                      CYCLOMALTODEXTRIN GLUCANOTRANSFERASE
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RESULT 4
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AC P39832; P76286;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
"-affinity zinc uptake system membrane protei
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Mada C., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                        IDENTIFICATION.
IDENTIFICATION.
MEDLINE=95075659; PubMed=7984428;
Paradovsky M., Rudd K.E., Koonin
Paradovsky M., Pubmed approach
                                                                            Patzer S.I., Hantke K.;
"The ZnuABC high-affinity zinc uptake system and Escherichia coli.";
Mol. Microbiol. 28:1199-1210(1998).
-I- FUNCTION: INVOLVED IN THE HIGH-AFFINITY ZINC
                                                                                                                                                                                                Borodovsky M., Rudd K.E., Koonin E.V.;
"Intrinsic and extrinsic approaches for detecting genes bacterial genome.";
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 80-261 FROM N.A. MEDLINE=88314937; PubMed=284
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-92 FROM N.A. STRAIN=K12 / EMG2; Robison K., O'Keeffe T., C
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                         <del>-</del>
                                                     +
                                                                                                                                                                                                                                                                                            "Structure and regulation of the Escherichia in DNA repair and recombination.";
J. Bacteriol. 170:4322-4329(1988).
                                                                                                                                                                                                                                                                                                                                       Shinagawa H., Makino K., Amemura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97251358;
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          SIMILARITY:
PROTEINS. ST
                                                   SUBCELLULAR LOCATION: Integral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
                                       (Probable).
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        TO THE ABC-3 SUBFAMILY OF D H.INFLUENZAE ZNUB.
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              "The nucleotide sequence of Drosophila 2.1-kb mRNA.";
                                                                                                                                                         MEDLINE=85240569; PubMed=2409449;
Emori Y., Shiba T., Kanaya S., Inou
"The nucleotide sequences of copia
virus-like particles.";
Nature 315:773-776(1985).
                                                                                                                                                                                                                                                                                                   Mount S.M., Rubin G.M.;

Mount S.M., Rubin G.M.;

"Complete nucleotide sequence of the Drosophila transposable element copia: homology between copia and retroviral proteins.";

Mol. Cell. Biol. 5:1630-1638(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPI ROME STANDARD; PRT; 1409 AA. P04146; Q03728; Q24280; Q24555; Q24585; Q2458 101-NOV-1986 (Rel. 03, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Copia protein [Contains: Copia VLP protein; C (EC 3.4.23.-)].
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EMBL; D90828; BAA15670.1; -.
EMBL; D90828; BAA15670.1; -.
EMBL; U38702; AAA81031.1; -.
EMBL; M21298; -; NOT ANNOTATED_CDS
EMBL; C64048. C6448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygo; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                      SEQUENCE FROM N.A. MEDLINE=89183629;
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  Acids Res. 17:2134-2134(1989)
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copia-related RNA
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                                             copia-specific
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pfam; PRO0098; zf-CCHC; 1.
pfam; PR00098; cZHCZNFINGER.
prints; pr00939; CZHCZNFINGER.
prosite; pr00141; ASP protease; PALSE_NEG.
pr0SITE; pS50158; ZF-CCHC; 1.
pr0SITE; pS50158; ZF-CCHC; 1.
pr0SITE; pS50158; ZF-CCHC; 1.
copia protease; Aff-binding; polymorphism; Zinc-finger.
polyprotein; Alternative splicing; Polymorphism; Zinc-finger.
copia vLP protein (POTENTIAL).
copia vLP protein (POTENTIAL).
copia vLP protease (POTENTIAL).
copia vLP protease (POTENTIAL).
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EMBL; X02599; CAA26445.1; -.
EMBL; X02500; CAA26446.1; -.
EMBL; X02600; CAA26447.1; -.
EMBL; X13719; CAA38197.1; -.
EMBL; X54147; CAA38086.1; -.
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autocatalytic processing.";
EMBO J. 9:535-541(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [4] SEQUENCE FROM N.A. (ISOFORM SHORT), AND MUTAGENESIS OF ASP-292.
                                                                                                                                                                                                                                                                                                                 ACT SITE VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shiba T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0013437; copia\GIP.
InterPro; IPR001969; Aspprotease.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90151630; PubMed=1689241; Yoshioka K., Honma H., Zushi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Larva;
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A03324; OFFFCP. MEROPS; All.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Virus-like particle formation of Drosophila copia through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBOId=P04146-2; Sequence=VSP_005226; SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY All. SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                          1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                             72
                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P04146-1; Sequence=Displayed;
                                                                                                                    24;
                                                                                                                                   Similarity
GDMTRMNNFKRYLMEKFRMTDLNEIKHFIGIRIEMOEDKIYL 1137
                             GESLKWN------VRNLDVMPIFETLALRLVLQGDVIWL 104
                                                          WFEVFEQALKECEFVN
                                                                                      WFQIED---NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYV--HADDVEFVP 71
                                                                                                                                                                               1289
292
191
300
866
1409
                                                                                                                                                                                                                                                                                     1265
                                                                                                                    Conservative
                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                                                                                                 270
1409
247
292
1374
                                                                                                                                                                                                          1409
292
191
300
                                                                                                                                                                                                                                                                                     1288
                                                                                                                                                                                              866
                                                                                                                                  11.4%;
                                                                                                                                                                             162817
                                                                                                                                                                          STTGYLFKMEDENLICWNTKRONS -> VQQGIYSKCLILI
SFYGIQRDBTQ (IN VARIANT COPIA-RELATED).
MISSING (IN VARIANT COPIA-RELATED).
D-A: LOSS OF ACTIVITY.
S -> N (IN REF. 2; CAA26447).
I -> V (IN REF. 2; CAA26447).
Q -> E (IN REF. 2; CAA26447).
Q -> E (IN REF. 2; CAA26447).
                                                                                                                    18;
                                                                                                                                  Score 72; DB 1; Length 1409; Pred. No. 13;
                                                                                                                                                                                                                                                                                                   Missing (in isoform Short).
/FTId=VSP_005226.
                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kondo S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site.
                                                          SSVDRCIY--ILDKGNINENIYVLLYVDDVVIAT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Togashi S., Miyake
                                                                                                                    34;
                                                                                                                     Indels
                                                                                                                     26;
                                                                                                                    Gaps
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RESULT 6
CDGT_BACOH
Matches
                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006589; Alp amyl_cat sub.
InterPro; IPR006048; Alpha_amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006044; GBD_4.
InterPro; IPR006044; Glyco_hydro_13.
InterPro; IPR002999; IPT_TIG.
Pfam; PF00128, alpha-amylase; 1.
Pfam; PF00188, CBM_20; 1.
Pfam; PF00686; CBM_20; 1.
Pfam; PF001833; TIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P27036;
01-AUG-1992 (Rel. 2
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
                                                                                          CHAIN
DISULFID
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and sequencing of a cyclodextrin glucamotransferase gene from Bacillus ohbensis and its expression in Escherichia coli."; Appl. Microbiol. Biotechnol. 35:600-605(1991).
-I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
-I- COPACTOR: BINDS TWO CALCIUM IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sin K.A., Nakamura A., Kobayashi K., Masaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=92000599; PubMed=1368710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus ohbensis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclomaltodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDGT_BACOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90243; BAA14289.2; -. HSSP; P31797; 1CYG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Cyclomalcodextrin glucanotransferase precursor
(Cyclodextrin-glycosyltransferase) (CGTase).
                                                                                                                                                                                                                                                                                   SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
                                                                                                                                                                                                                                                                                                                         PRINTS; PR00110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
SMART: SM00642: Asmv: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1481;
                                                                                                                                                                                                                                                               Iransferase; Glycosyltransferase; Calcium; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANBOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONI IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNOWN AS THE ALPHA-AMYLASE FAMILY.
                      Similarity
                                                                                            704 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                     704
704
75
251
279
                                                                                               78621 MW;
                      11.2%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales;
21;
Score 70.5; DI
Pred. No. 8.7;
21; Mismatches
                                                                                          CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 04FA14951D5ACECB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                             DB 1;
  44;
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                                             Length 704;
     Indels
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     13;
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       Gaps
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12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP

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RESULT 7
US30_HCMVA
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                                                                                                                                                                      Matches
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Best Local (
                                                                                                                                                                                                                         EMBL; X17403; CAA35262.1; -.
EMBL; X04650; CAA28340.1; -.
PIR; E27216; QQBED5.
Hypothetical protein.
CARBOHYD 75 75
CARBOHYD 98 98 N
CARBOHYD 140 140 N
SEQUENCE 349 AA; 39114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989
01-MAR-1989
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the EMUropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINB=90269039; PubMed=2161319;
Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87169717; PubMed=3031311; Weston K., Barrell B.G.; "Sequence of the short unique region,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P09706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein HHRF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeats of human cytomegalovirus."; ol. Biol. 192:177-208(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCMVA
 201
                                                       141
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                                                                                   50
                                                                                                              81
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                                                                                                                                                                                  Similarity
                                                                                KADY-GGVGENLYVHADDVEF------VPGESLKWNV----
                                                                                                            QCRLRNGATFSKGDIEGNFSGPVVVELDYEDIDITGERQRLRFHLSGLGCPTKENIRKDN 140
GKNAEVPPATRTSSTYSVLSAFVVWI 226
                                                       ESDVNGGIRWALYIQTGDAKYGIRNQHLSIRLMYPGEKNTQQLLDSDFSCERHRRPSTPL 200
                                                                                                                                        RCYIDNGKLFARGSIVGNMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEDSIYRNLYDLADYDLNNTVMDQYLKESIKLWLDKGIDGIRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GE-SLKWNVRNLDVMPIFETLALRLVLQGDVIWL-RCVPELRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPNHSSPALETDPSYAENGAVYNDGVLIGNYSN---DP----
                         -RNLDVMPIFETLALRLVLQGDVIWL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 10, Created)
(Rel. 10, Last sequence update)
(Rel. 17, Last annotation updat
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                          140 N
; 39114 MW;
                                                                                                                                                                                11.0%;
                                                                                                                                                                      16;
                                                                                                                                                                                                                            N-LINKED (GLCNAC. ...
N-LINKED (GLCNAC. ...
N-LINKED (GLCNAC. ...
W; 613013B517DED750 (
                                                                                                                                                                               Score 69.5; DI
Pred. No. 4.9;
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                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349
                                                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                              DB 1;
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                                                                                                                                                                     36;
                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                              Length 349;
                                                                                                                                          RFVF----
                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration -
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RESULT

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Best Local S
Matches 15
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Mao Y., Xie Y., Jiang M.;

"CDNA Cloning of a novel human F-box protein.";

"CDNA (LOning of a novel human F-box protein.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

-1- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
uridylyltransferase) (UDP-glucose--hexose-1-phosphate
                                                                                                                                                                                                                                                         GAL7_CRYNE STA
P40908;
01-FEB-1995 (Rel.
         promoter.";
Mol. Microbiol. 16:1099-1109(1995).
-i- CATALYTIC ACTIVITY: UDP-glucose
                                                                                                                                   Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidio
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch)
                                                                  SEQUENCE FROM N.A.
MEDLINE=96020643; PubMed=8577246;
Wickes B.L., Edman J.C.;
                                                                                                                      NCBI_TaxID=5207;
                                                                                                                                                                                        uridylyltransferase).
                                                                                                                                                                                                                                                                                                  CRYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF453435; AAN76812.1; InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
-!- SIMILARITY: Contains 1 F-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-box only protein 16. FBX016 OR FBX16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8IX29;
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                     "The Cryptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conjugation.
CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose alpha-D-glucose 1-phosphate + UDP-galactose
                                                                                                                                                                                                                                                                                                                                                       211
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                                                                                                                                                                                                                                                                                                                                                                                                          15; Conserv
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                                                                                                                                                                                                                                                                                     STANDARD;
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                                                      neoformans GAL7
                                                                                                                                                                                                                                                        31, Created)
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Last annotation update)
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Pred. No. 4.5;
4; Mismatches
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                                                     gene
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                                                        use
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                                                                                                                                                 Heterobasidiomycetes;
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              1-phosphate
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Best Local S
Matches 21
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P78325;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAM 8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 8) (Cell surface antigen MS2) (CD156a antigen) (CD156).
ADAM8 OR MS2.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001937; Galp_UDPtransf1.
InterPro; IPR005851; Galp_Utransf 1.
InterPro; IPR005859; Galp_Utransf_N.
InterPro; IPR005849; Galp_Utransf_N.
Pfam; PP002744; Galp_UDp_transf; 1.
Pfam; PP01087; Galp_UDptransf1; 1.
ProDom; PD005051; Galp_UDptransf1; 1.
                       TISSUE=Blood;
MEDLINB=97271556; PubMed=9126482;
Yoshiyama K., Higuchi Y., Kataoka M., Matsuura K., Yamamoto S.;
"CD156 (human ADAM8): expression, primary amino acid sequence, gene location.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metal-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Nucleotidy Itransferase; Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the galactose-1-phosphate uridylyltransferase family 1.
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2S00117; GAL P U
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Pred. No.
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78)
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-I- COPACTOR: Binds 1 zinc ion per subunit (Probable).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- TISSUE SPECIFICITY: EXPRESSED ON NEUTROPHILS AND MONOCYTES.
-I- SIMILARITY: Belongs to peptidase family M12B.
-I- SIMILARITY: Contains 1 disintegrin domain.
-I- DATABASE: NAME=PROW; NOTE=CD guide CD156 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd156.htm".
                                                                                                                                                       DISULFID
CARBOHYD
CARBOHYD
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ACT SITE
METAL
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InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50215; ADAM MEDRO; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS0142; ZING PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 602267; -.
GO; GO:0005888; C:proteoglycan integral to plasma membrane; InterPro; IPR006586; ADAM cysteine.
InterPro; IPR001762; Disintegrin..
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Genew; HGNC:215; ADAM8.
MIM; 602267; -.
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SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D26579; BAA05626.1; HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR002870; Pep M12B propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR0016025; Zn_MTpeptdse.
InterPro; IPR006025; Zn_MTpeptdse.
                                                                                                                                              SEQUENCE
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                                        151
60 -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
                                                                                          29;
                                                                                                        Similarity
                                     RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV
                                                                 KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN---
                                                                                                                                                                                                                                                                                                                                                                                  Metalloprotease; Zinc; Signal; Glycoprotein;
                                                                                                                                             824 AA;
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334
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Pfam; PF00083; sugar_tr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92234930; PubMed=1569007; ISland M.D., Wei B.-Y., Kadner R.J.; Island M.D., Wei B.-Y., Kadner uhp genes "Structure and function of the uhp genes transport system in Escherichia coli and J. Bacteriol. 174:2754-2762
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or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
INDUCTION: EXTERNAL GLUCOSE-6-PHOSPHATE INDUCES THE EXPRESSION
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RX Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,

RA Chillingworth T., Comnor R., Devlin K., Gentles S., Hamlin N.,

RA Harris D.B., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,

RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,

RA Moule S., Smith V., Walsh S., Whitehead S., Barrell B.G.;

"The nuclectide sequence of Saccharomyces cerevisiae chromosome IX.";

RI Nature 387:84-87(1997).

C. -- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS

CC OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS (POTENTIAL).

CC OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS (POTENTIAL).

CC --- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

C--- SUBCELLULAR LOCATION: Integral membrane protein.

CC --- SUBCELLULAR LOCATION: the cation transport ATPases family (P-type CC ATPases). Subfamily IV.
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                          or send an email to license@isb-sib.ch).
                                       entities requires a license agreement
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EMBL; Z38060; CAA86174.1;

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InterPro; IPR005539; Flippase.
InterPro; IPR005534; Hydrolase.
Pfam; PF00122; E1-E2 ATPase; 1.
PFAM; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
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TIGRFAMS; TIGR01494; ATPase_P-type;
PROSITE; PS00154; ATPASE_E1_E2; 1.
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SGD;
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MEDLINE-22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;

"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8D$33;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                 Proc.
                                                                                                                                                                                                                                                                                                                                                                       pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
                                                                                                                                                     SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the adenylate kinase family.
                             ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRMU
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S0001310; NEO1.
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PHOSPHORYLATION (PROBABLE).
W; DC7225CC9577DBE6 CRC64;
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   There are no restrictions 
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Best Local (
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Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;

Palinuroidea; Palinuridae; Panulirus.

NCBI TaxID=6737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLNA PANAR
Q04831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANAR
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NP_BIND 7 15 ATP (BY SIMILARITY).

SEQUENCE 212 AA; 23638 MW; 5AF9ClAD9B5D5520 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE015024; AAN59609.1; -- HAMAP; MF_00235; -; 1. Pfam; PF00406; ADK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homooctamer.
-!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein related to eukaryotic glutamine synthetase. Gene 129:275-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Olfactory organ;
MEDLINE=93314973; PubMed=8100791;
Trapido-Rosenthal H.G., Linser P.J., Greenberg R.M., Gleeson R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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PROSITE; PS00113; ADENYLATE_KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000657; Adenylate_kin; 1.
                                                                                                                                                                                                                        EMBL; M96798; AAA02583.1; -. PIR; JN0716; JN0716.
                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr W.E.;
                            ProDom; PD001057; Gln_synt_C; 1.
PROSITE; PS00180; GLNA_1; 1.
                                                                                InterPro; IPR001691; GLN_synth.
InterPro; IPR001637; GlnA_adenyltn.
Pfam; PP00120; gln-synt; I.
Pfam; PP03951; gln-synt_N; 1.
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O THE GLUTAMINE SYNTHETASE FAMILY
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                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q935W0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
"""" an a sium-chelatase 67 kDa subunit (Mg-protoporphyrin IX chelatase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligase.
SEQUENCE
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D., Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20433266; PubMed=10976061;
Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
"Molecular evidence for the early evolution of photosynthesis.";
Science 289:1724-1730(2000).
             EMBL; AY005135; AAG12406.1; -.
EMBL; AE012889; AAM72526.1; -.
TIGR; CT1296; -.
                                                                                                                                                                                                                                                                                                            photosynthetic, anaerobic, green-sulfur bacterium.";
proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
-!- FUNCTION: Involved in bacteriochlorophyll biosynthesis; introduces
a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlorobium tepidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=TLS / ATCC 49652 / DSM 12025; MEDLINE=22103685; PubMed=12093901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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                                                                                                                                                                                                                                     PATHWAY: Bacteriochlorophyll biosynthesis.
SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
SIMILARITY: Contains 1 VWFA domain.
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IPR000523; Mg_chelatse_chII.

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Search completed: January 22, 2004, 11:39:40 Job time: 19.4198 secs
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Best Local :
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                              Pfam; PF01078; Mg chelatase; 1.

Pfam; PF00092; vwa; 1.

PROSITB; PS50234; VWFA; 1.

PROSITB; PS50234; VWFA; 1.

Photosynthesis; Bacteriochlorophyll biosynthesis; Complete proteome.

Photosynthesis; Bacteriochlorophyll biosynthesis; Complete proteome.

DOMAIN 277 329 GLU/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002035; VWF_A.
                                                                                                                                             401
                                                                       455 VASLLQNAYVHRDQVSLISFRGKQAQVLLPPSQSVDRAKRELDVLP 500
                                                                                                          53
                                                                                                                                                                                                                 31;
                                                                                                                                                                              ω
                                                                                                                                                                                                                                  Similarity
                                                                                                                                             EQAKKGIKSTAALIIGKD---DIKIKRFRDKSGTLFIFMVDASGSMALNRMR----QAKGA 454
                                                                                                                                                                       EDALRPWKSTA-----KHPWFQIEDNRCYIDNGKLF-----ARGSIVGNMSRFVFDPKAD 52
                                                                                                       YGGVGENLYVHADDVEFV------PGESLKWNVRNLDVMP 86
                                                                                                                                                                                                                                                                                      620 AA;
                                                                                                                                                                                                                                                                                                        432
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                          620
                                                                                                                                                                                                                                                                                      67015 MW;
                                                                                                                                                                                                                10.5%; Score 66; DB 1; Length 620; 29.2%; Pred. No. 23; tive 10; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                        VWFA.
                                                                                                                                                                                                                                                                                      05BE07DD3D96F917 CRC64;
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                        740
117.5
                                              110
109.5
106.5
106.5
                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
100.0
78.1
12.4
11.6
11.6
11.2
11.2
11.2
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947
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                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                     SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

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(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

(SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _Geneseq_19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                                                                                                       Length DB
                                           498
1189
354
354
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                     AAY97248
ABG31298
ABG31300
AAW47008
AAB10640
AAB10641
AAE05128
  ABG31502
                                                                                                                                                                                         AAY97249
                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Search time 64.6382 Seconds (without alignments) 434.644 Million cell updates/sec
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Human VEGF-X prote
Human VEGF-X prote
Infectious salmon
Muscarinic acetylc
                                                                                     Cytomegalovirus US
Cytomegalovirus US
Hydrophobic protei
Hydrophobic protei
Glutathione-S-tran
                                                                                                                                                                                                                                     Description
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ALIGNMENTS

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RESULT 1
AAY97249
 Chimeric - Human cytomegalovirus.
Chimeric - Apis sp.
Chimeric - Homo sapiens.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                AAY97249;
10-AUG-2000.
                                                 Peptide
                                                                      Misc-difference
                                                                                           Protein
                                                                                                                         Key
                                                                                                                                                                                               US2; hCMV; major histocompatibility complex; MHC; class I; class antigen presentation; inhibition; CD8-positive; CD4-positive; T ctransplant; gene therapy; immunosuppressive; fusion; DL6.
                                                                                                                                                                                                                                       Cytomegalovirus US2t-DL6 fusion protein.
                                                                                                                                                                                                                                                           DEC-2000
                                                                                                                                                                                                                                                                                                     AAY97249 standard; Protein; 177
                   WO200046361-A1.
                                                                                                             Peptide
                                                                                                                                                                                                                                                           (Mirst entry)
                                                                                            /label= Bee_mellitin_signal_peptide
22..157
                                                                                                                        Location/Qualifiers
                                     /label= DL6_epitope
                                                           note= "Single glycine spacer"
                                                                                'label= Soluble_US2_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            effect on the MHC class II pathway, inhibiting recognition of cellular tissue by CDB-positive and CDA-positive T cells. US2 or its soluble variants, can be used to reduce inappropriate immune responses. The US2 protein can be used to improve the persistence of a virus. Vectors encoding soluble US2 protein (residues 28-143) can be used to treat autoimmune disease, especially where it is mediated by MHC II molecules. The vector can also be used to improve gene therapy, and preferably also contains a sequence encoding a therapeutic product. The protein is exogenously supplied or expressed from a recombinant cell, and may also be used to inhibit CD4-positive mediated immune responses, transplant immune responses and gene therapy
                                                               US2; hCMV; major histocompatibility complex; MHC; class I; class II; antigen presentation; inhibition; CD8-positive; CD4-positive; T cell; transplant; gene therapy; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytomegalovirus (hCMV) US2 protein, which has previously been shown to block the major histocompatibility complex (MHC) class I antigen presentation pathway, blocks the MHC class II pathway. The US2 protein does not have to be mutated to cause inhibition of the MHC class II pathway. The binding domain recognizes MHC I heavy chains, MHC II alpha chains, and optionally DM-alpha chains. US2 has a double inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting recognition of cellular tissue by CD8+ and CD4+ T cells, treat or prevent autoimmune diseases, and to improve gene therapy, comprises introducing human cytomegalovirus US2 protein into cells
                                  Human cytomegalovirus
   WO200046361-A1
                                                                                                                                Cytomegalovirus US2 protein
                                                                                                                                                                    04-DEC-2000
                                                                                                                                                                                                  AAY97248;
                                                                                                                                                                                                                                 AAY97248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; Page 49; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune responses.
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                                                                                                                                                                                                                                                                                                                                                                                                     LFARGSIVGNMSRFVFDFKADYGGVGENLYVHADDVEFVFGESLKWNVRNLDVMFIFETL
                                                                                                                                                                                                                                   standard; Protein; 199 AA
                                                                                                                                                                                                                                                                                                                                                   ALRIVLQGDVIWLRCVPELRVDYTSSAYMWNMQYGMVGQPELAPEDPEDSALLEDPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKFLVNVALVFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                                  (first entry)
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Pred.
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No. 7.9e-99;
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RESULT 3
ABG31298
ID ABG3
XX
AC ABG3
XC ABG3
XX
DT 21-C
XX
DE Hydr
XX
KW Sigr
KW Sigr
KW trar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the human cytomegalovirus (hCMV) US2 protein, which has created by been shown to block the major histocompatibility complex (MHC) class I antigen presentation pathway, blocks the MHC class II pathway. The US2 protein does not have to be mutated to cause inhibition of the MHC class II pathway. The binding domain recognizes MHC I heavy chains, and optionally DM-alpha chains. US2 has a double inhibitory effect on the MHC class II pathway, inhibiting recognition of cellular tissue by CD8-positive and CD4-positive T cells. US2 or its soluble variants, can be used to reduce inappropriate immune responses. The US2 protein can be used to improve the persistence of a virus. Vectors encoding soluble US2 protein (residues 28-143) can be used to treat autoimmune disease, especially where it is mediated by MHC II molecules. The vector can also be used to improve gene therapy, and preferably also contains a sequence encoding a therapeutic product. The protein is exogenously supplied or expressed from a recombinant cell, and may also be used to inhibit CD4-positive mediated immune responses, transplant immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
               polytopic membrane protein; G protein-coupled receptor;
                 transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase; G protein-coupled receptor; transporter protein.
                                                                      Signal sequence; ligand identification; hydrophobic protein;
                                                                                                          Hydrophobic protein mellitin tag tag-Human beta2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting recognition of cellular tissue by CD8+ and CD4+ T cells, treat or prevent autoimmune diseases, and to improve gene therapy, comprises introducing human cytomegalovirus US2 protein into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA53813.
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                                                                                                                                                21-OCT-2002
                                                                                                                                                                                                                        ABG31298 standard;
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                                                                                                                                                                                                                        Protein; 451
                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.1%; Score 740; DB 21;
100.0%; Pred. No. 2.5e-75;
tive 0; .Mismatches 0;
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Synthetic.

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UXAXEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-EB tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EB tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents the hydrophobic protein mellitin tag tag-Human beta2-adrenergic receptor EE used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel method for identifying a ligand for hydrophobic protein. The method comprises selecting a ligand molecule affinity selection by exposing a hydrophobic target protein bound by amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand
Signal sequence; ligand identification; hydrophobic protein; transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase;
                                                                          Hydrophobic
                                                                                                           21-OCT-2002
                                                                                                                                              ABG31300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                              ABG31300 standard; Protein; 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                    121 ALRLVLQGDVIWLRCVPELRVDYTSSAY 148
                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                              61 LFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS, Annis DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEOGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                             MKFLVNVALVFMVVYISYIYADYKDDDDKMGQP---------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKFLVNVALVFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGK 60
                                                                                                                                                                                                                                                                      IVLAIVEGNVLVITAIAKFERLQTVTNY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 AA;
                                                                      protein mellitin-flag @Tag-human m1 mAChR-EE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                         (first
                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%; Score 117.5; DB 2
27.7%; Pred. No. 0.00022;
tive 13; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalghatgi K,
                                                                                                                                                                                 ያ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nash
                                                                                                                                                                                                                                                                                                                                           ·HAPDHDVTQQRDEVWVVG----MGIVMSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a ligand for
gand molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 5
AAW47008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc amphiphile to a multiplicity of molecules to promote formation of at cleast a complex between the hydrophobic target protein and the ligand cc molecule, separating the complex from the unbound molecules, and cc identifying the ligand molecule. The method of the invention is cusful for identifying a ligand for hydrophobic protein such as a cmembrane, integral membrane, transmembrane, monotopic or polytopic cc membrane, pump, channel, receptor kinase, G protein-coupled receptor, cc or transporter protein, or membrane-associated enzyme, or Myc tag-EE cc tag-human m2 mAChR, flag tag-human beata adrenergic receptor-EE tag, cc tag-human neurokinin 3 receptor-HSV tag-Myc tag-flag tag-human m1 mAChR-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel cc medicines and medicinal diagnostics. The present sequence represents hydrophobic protein mellitin-flag @Tag-human m1 mAChR-EE used in the cc method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a nover mercane comprises selecting a ligand molecule by hydrophobic protein. The method comprises selecting a ligand molecule by affinity selection by exposing a hydrophobic target protein bound by an affinity selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection of at a selection
                                                                                                                                                Synthetic.
                                                                                                                                                                                                          Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprote
                                                                                                                                                                                                                                                                                                Glutathione-S-transferase and hTRT fusion protein 8.
                                                                                                                                                                                                                                                                                                                                                              13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW47008 standard; Protein; 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000US-258970P.
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                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-599728/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felsch JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUL-2002
                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKFLYNVALVFMVVYISYIYARLPDGITKAGEDA------LRPWKSTAKHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKFLVNVALVFMVVYISYIYADYKDDDDKMNTSAPPAVSPNITVLAP----GKGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%;
nilarity 51.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498 AA;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
Location/Qualifiers
22..23
/note= "enterokinase cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 0.0018;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                             ribonucleoprotein.
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                                                                                                                                                                                                                                                                                                        of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; the protein or polymucleotide, on administration of the compound; (C) preparation of frecombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of the hTRT RNA or protein in a sample by binding a relevant or protein complex or amplification product with presence of hTRT in the sample; and (D) increasing the product and correlating the presence of the propersion; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding the fraction of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase.
                                                                                                                                                                                  Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 234-235; 387pp; English.
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                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews WH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-1997
                                                                                                                                                                                                                                                                                              activity. A protein preparation of hTRT can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L4-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a fusion
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UNIV 1
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                                                                                                                                                                                                    Similarity
                                                             RAPRCRAVRSLLRSHYREVLPLATFV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV
                                                                                         EDNRCYIONGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF------V
                                                                                                                                                     MKFLVNVALVFMVVYISYIYARLPDGITKAG--EDA-----LRPWKSTAKHPWFQI
                             PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                        MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP
                                                                                                                                                                                                                                                  1189 AA;
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                                                                                                                                                                                      Conservative
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97US-0844419.
97US-0846017.
97US-0851843.
WDARPPPAAPSFROVSCLKELVARVLORLC
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97US-0911312.
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                                                                                                                                                                                                    11.6%;
32.1%;
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Harley
                                                                                                                                                                                      10;
                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                    Score 109.5; DB Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein from an example
                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                    65;
146
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                                                                                                                                                                                      Indels 31;
                                                                                                                                                                                                                   Length 1189;
                                                                                                                                                                                                                                                                                                 in the new
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
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RESULT 6

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                                                                                                                                                                                                                                                                This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vilnerary, cytostatic, and its encoding polynucleotide (IIa) which has antinerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and cartifiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating corporating cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate eascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products further invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein which is can be expressed in Baculovirus/insect cell systems and which is
                                                                                                                                         Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon RD, Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 20; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA71984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10640 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-442669/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JANC ) JANSSEN PHARM NV
 36
                               61 LFARGSIVGNMSRFVFDFKADYGGVGE------NLYVHADDVEFVPGESLKWNVR 109
                                                                                                                                                           Similarity
                                                                                                    MKFLVNVALVEMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGK 60
                                                                                                                                                                                                                                                 in the method of the
                                                                                                                                                                                                              354 AA;
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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99US-0124967.
99US-0164131.
----SKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSP--
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                                                                                                                                                           11.2%;
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                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
                                                                                                                                           Score 106.5;
Pred. No. 0.00
L4; Mismatches
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                                                                                                                                                                                                                                                     invention.
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                                                                                                                                                             .0028;
                                                                                                                                                                            DB 21;
                                                                                                                                            41;
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                                                                                                                                            Indels
                                                                                                                                                                             Length
                                                                                                                                                                               354;
                                                                                                                                            81;
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NLDVMPIFETLALRIVLQGDVIWLRCVPELRVDYTSSAYMWNMQYGMVGQPELAPEDPED

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RESULT 7
AAB10641
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Matches
                                                   Query Match
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                 This invention describes a novel vascular endothelial growth factor-X (VZGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate rescularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote this result are treating to the invention are useful as the content of the content of the content of the content of the products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, and burns and to promote the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content 
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                                                                                                      Sequence
                                                                                                                                                                       skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promobing angiogenic activity or vascularization. This sequence represents a human VEGF-X protein which can be expressed in E. coli systems and which is described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon RD,
Dhanaraj SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human VEGF-X protein for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JANC ) JANSSEN PHARM NV.
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-442669/38.
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     44;
                                                                                                                                                       invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPHTYPRNTVLVWRLVAVEENVWIQLT----
                                                                                                      354
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                            11.2%; Score 106.5; DB 24.4%; Pred. No. 0.0028;
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14;
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     Mismatches
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  41;
                                                   21;
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     Indels
                                                Length
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     81;
  Gaps
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Indels

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Matches 23
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N-PSDB;
                                                                                                                                                      The present invention relates to vaccine for prevention and/or prophylaxis of infectious salmon anaemia in fish. The invention prophylaxis of infectious sequence encoding viral proteins of infectious salmon anaemia virus (ISAV) as well as the isolated protein. Nucleic acids encoding viral protein is useful for the manufacture of a DNA vaccine for diagnosis, treatment and/or prophylaxis of infectious salmon anaemia in fish, and viral protein can be used for the manufacture of antibodies that are specific for ISAV. The present sequence is infectious salmon anaemia virus 9Z-M fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 39-41; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel vaccine for treatment and/or prevention of infectious salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biering E,
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29-FEB-2000;
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                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 386
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                                                                                                           386
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llarity 59.0%;
Conservative
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2000EP-0200700.
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Score 104; DB 2.
Pred. No. 0.006;
5; Mismatches
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                                                        DB 22;
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                                                        Length 386;
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밁
                                                                                                                           Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for identifying a ligand for a hydrophobic protein. The method comprises selecting a ligand molecule by affinity selection by exposing a hydrophobic target protein bound by an amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-EE tag-human meurokinin 3 receptor-HSV tag-Myc tag, flag tag-human beta2 addrenergic receptor-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents the protein sequence of muscarinic acetylcholine receptor in a baculovirus expression vector used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal sequence; ligand identification; hydrophobic protein;
transmembrane protein; monotopic membrane protein;
polytopic membrane protein; pump; channel; receptor kinase;
G protein-coupled receptor; transporter protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscarinic acetylcholine receptor protein in Baculovirus expression.
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                                                                                                                                                                                                                                                          Sequence
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                                                                                                                               . Similarity 22; Conserv
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                                                       MKFLVNVALVFMVVYISYIYARLPD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 45; 97pp; English.
                                                                                                                                                                                                                                                                 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annis DA,
                                                                                                                               Conservative
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                                                                                                                                                          Score 104; DB 23
Pred. No. 0.0084;
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                                                                                                                                                                                                DB 23;
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                                                                                                                                                                    CC to express leech active polypeptides. The active polypeptide has CC a molecular weight of 7000-17,000 Da (as measured by mass complementry), and is derived from ectoparasitic leeches, of order (Rhynchobdellida, of genus placobdella and especially of species P. papillifera. The polypeptide inhibits the alternate route of CC complement activation but has substantially no effect on complement activation but has substantially no effect on complement complement factor D and/or C3bBb complex. The active polypeptide is CC useful for manufacturing a medicament and inhibits one or more steps in the alternate pathway of complement activation. It is useful for treating or preventing conditions, such as haemodialysis and CC extra-arterial stents, rejection of transplanted organs or tissues active such as the presence of in-dwelling catheters and CC extra-arterial stents, rejection of transplanted organs or tissues of complement activation activations of tissues by reperfusion after an ischaemic period and other conditions associated with activation of complement, including anaphylaxis, associated with activation of alternate complement pathway in a cathetic activation of alternate complement pathway in a
                                                             Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides from the leech Placobdella papillifera which inhibit alternate pathway of complement activation, useful for treating rheumatoid arthritis, sepsis, asthma involving alternate complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-522011/57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Active polypeptide; ectoparasitic leech; Rhynchobdellida; C3bBb complex; complement activation; complement factor D; haemodialysis; catheter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal peptide of bee venom melittin.
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                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a signal peptide, which may be used to express leech active polypeptides. The active polypeptide has
                                                                                                                                                         patient.
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                                                               21;
                                                                              Similarity
                     MKFLVNVALVFMVVYISYIYA 21
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                                                                              Score 102; ; Pred. No.
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                                                                Mismatches
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                                                                                                DB 22;
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RESULT 10

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ABG31292
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Signal sequence; ligand identification; hydrophobic protein; transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase;
                                                                                                                 Heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor in the presence of UGGT -
                                                                                                                                                                         21-OCT-2002
                                                                                                                                                                                                                                                                                  ABG31292 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-2000; 2000WO-CA00883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; honeybee;
melittin signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melittin signal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention relates to a method for determining the effect of a
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DB; AAF60733.
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                                                                                                              signal
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-EE tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for identifying a ligand for hydrophobic protein. The method comprises selecting a ligand molecule affinity selection by exposing a hydrophobic target protein bound by amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a method of identifying a ligand for hydrophobic protein such as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention and the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention as a method of the invention and the invention and the invention and the invention and the invention and the invention and the invention and the invention and the invention and the invention and the inventio
                                                                                                                                                                                  Honeybee; melittin; signal sequence; immunoglobulin; B-cell lymphoma; B-cell mediated pathology; cytostatic; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antidiabetic; antithyroid;
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                                                                                                                                                        autoimmune disease.
                                                                                                                                                                                                                                                                                                                Honeybee melittin signal sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB10034 standard; Protein; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 10.8%; Score 102; DB 23; Similarity 100.0%; Pred. No. 0.00019; 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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WO200213862-A2 Apis melifica.

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents the honeybee melittin signal sequence, used in the invention to maximise secretion of heterologous proteins from insect cells. The invention relates to a novel composition for altering a B-cell mediated pathology in a patient. The composition for altering can be recomposition for altering a B-cell composition comprising at least a portion of a variable region of heavy chain or light chain (VH or VL) linked to at least a portion of an immunoglobulin constant region, where VH or VL region is associated with a B cell clone from the patient having the B cell mediated pathology. The composition of the invention has cytostatic, immunosuppressive, composition of the invention has cytostatic, immunosuppressive, and antithyroid activity. The composition is a vaccine useful for altering a B cell mediated pathology. This includes B cell jymphoma e.g. non-Hodgkins lymphoma, refractory low grade or follicular B cell lymphoma, autoimmune disease e.g. multiple sclerosis, systemic lupus erythematosus, anti-Hu associated paraneoplastic neurological syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-2000; 2000US-224722P.
11-AUG-2000; 2000US-224723P.
23-MAR-2001; 2001US-279079P.
                                                      Honeybee; signal sequence; rheumatoid arthritis; melittin; Vbeta; Valpha; T cell receptor; TCR; cytostatic; neuroprotective; antidabetic; dermatological; antirheumatic; immunosuppressive; antiinflammatory; antiarthritic; antithyroid; T cell lymphoma; autoimmune disease; multiple sclerosis; systemic lupus erythematosus; diabetes; inflammatory bowel disease; myasthenia gravis; thyroiditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune hepatitis, Type I diabetes, autoimmune thyroiditis and scleroderma. The pathology is treated by administering the composition to the patient, preferably with a cytokine e.g. granulocyte-macrophage-colony stimulating factor (GM-CSF) or chemokine e.g. monocyte chemotactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Page 17; 100pp; English
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                    Apis melifica
                                                                                                                                                                                              Honeybee
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                                                                                                                                                                                                                                                                                                            AAU76918 standard; Peptide; 21
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                                                                                                                                                                                              melittin signal sequence
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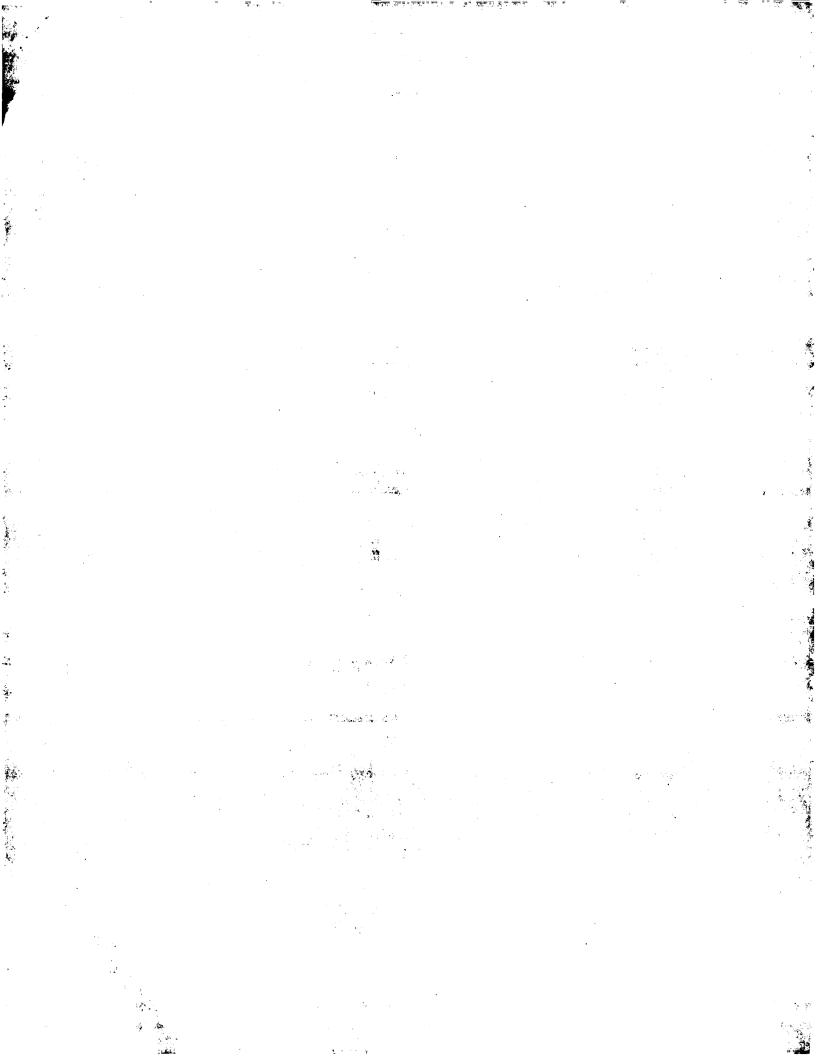
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RESULT 15
AAM52328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a method for altering a T cell mediated CC pathology in a parient, the method involves administering a composition comprising a chimaeric protein which comprises at least a portion of a CC comprising a chimaeric protein which comprises at least a portion of a CC vbeta or Valpha region of a T cell receptor (TCR), and at least a CC vbeta or Valpha region is associated with a particular TCR from a T cell from the CC valpha region is associated with a particular TCR from a T cell from the CC cytostatic, neuroprotective, antidiabetic, dermatological, CC cytostatic, neuroprotective, antidiabetic, dermatological, CC cytostatic, immunosuppressive, antidiabetic, dermatological, CC antithyroid activities. The composition of the invention is useful for CC altering a T cell mediated pathology in a patient, where the T cell composition of the invention is useful for CC mediated pathology is T cell lymphoma, or an autoimmune disease selected CC inflammatory bowel disease, myasthenia gravis, rheumatold arthritis, and CC thyroiditis. The present sequence represents the honeybee mellitin CC into maximise the secretion of heterologous proteins from transfected control maximise the secretion of heterologous proteins from transfected control maximise the secretion of heterologous proteins from transfected control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control c
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11-AUG-2000;
01-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Altering T cell mediated pathology in patient, involves administering composition having chimeric protein which has portion of Vbeta/Valpha
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                                                                                                                                                                                                         Honeybee melittin signal peptide #1
                                                                                                                                                                                                                                                   28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region of T cell receptor and portion of immunoglobulin constant
                                                                                                                      Apis melifica.
                                                                                                                                                                Honeybee; signal
                                                                                                                                                                                                                                                                                             AAM52328;
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                                                                                                                                                                                                                                                                                                                                      standard;
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; 2000US-224723P.
; 2001US-266133P.
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21-MAR-2000; 2000JP-0078897.

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                                                                                                                                                                                                                                                                                                         The present invention relates to an expression cassette for executing or promoting the expression of a structural gene. The expression cassette comprises a promoter connected to said structural gene and a secretion signal peptide which is arranged upstream of the structural gene. The present sequence is a signal peptide, which was used in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                A nucleic acid for promoting the expression of genes, comprises a secretion signal from chicken lysozyme or SF162 type human immunodefficiency syndrome virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-003332/01.
N-PSDB; AAI71796.
                                                                                                                                                                                                                                           invention.

Note: the present sequence is the SEQ ID 8 as given in the sequence listing. This sequence differs from the SEQ ID 8 given on page 8 (see AAM52506).
                                                                                                                                                                                                         Sequence
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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CARBOHYD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90269039; PubMed=2161319; Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G. "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                      EMBL; X17403; CAA35314.1; -.
EMBL; X04650; CAB37097.1; -.
EMBL; M18921; AAA45958.1; -.
PIR; FZ6078; QQBEC6.
Early protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "An enhancer element in the short unique cytomegalovirus regulates the production immediate early transcripts."; Virology 162:406-416(1988).
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Weston K., Barrell B.G.;
Weston K., Edricell B.G.;
"Sequence of the short unique region, short repeats,
long repeats of human cytomegalovirus.";
J. Mol. Biol. 192:177-208(1986).
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NCBI_TaxID=10360;
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Lruses; dsDNA viruses, no RNA stage; Herpesviridae;
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       NMSRFVFDPKADYGGVGENL-----YVHADDVEFVPGESLKWNV----
                                                         VLVLAILAVLFLRLADSVPRPLDVVV----SEIRSAHFRVEENQCWFHMGMLYFKGRMSG
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Pred. No. 3.8e-05;
6; Mismatches 56
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Apis cerana (Indian honeybee).
Eukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
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SPECIES=A.mellifera;
Barnham K.J., Hewish D., Werkn
Bartone N., Norton R., Rivett
Submitted (JUN-1998) to the PI
                                                                                                                                                                                                                                                                                                                       Schroeder E., Luebke K., Lehmann M., Beetz I.; "Haemolytic activity and action on the surface tension of solutions of synthetic melittins and their derivatives."; Experientia 27:764-765 (1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=83287387; PubMed=6309516;
Vlasak R., Unger-Ullmann C., Kreil G.,
"Nucleotide sequence of cloned cDNA co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apidae; Apis.
NCBI_TaxID=7460, 7461;
                                                                        Terwilliger T.C., Eisenberg D.; "The structure of melittin. II. In J. Biol. Chem. 257:6016-6022(1982)
                                                                                                                                                                                                                                   Luebke K., Matthes S., Kloss G.;
"Isolation and structure of N 1-formyl melittin.";
Experientia 27:765-767(1971).
                                                                                                                                                                                                                                                                                  SYNTHESIS.
SPECIES=A.mellifera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 44-69 (MELITTIN 1 AND SPECIES=A.mellifera;
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                                                                                                                                    X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                      Kreil G.;
                                                                                                                                                                                                SPECIES=A.cerana;
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                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=A.mellifera;
                                                                                                                                                                                                                                                                                                                                                                                                                                             'Sequence analysis of melittin from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepromelittin.";
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                                                                                                                                                           of melittin isolated from 33:241-244(1973).
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                            Kirkpatrick A.,
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28-FEB-2003
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Biochim. Biophys. Acta 1031:143-161(1990).

-i- FUNCTION: Main toxin of bee venom with strong hemolytic activity.

Integrates into cell membranes and has multiple effects, probably,
as a result of its interaction with negatively charged
phospholipids. It inhibits well known transport pumps such as the
Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
permeability of cell membranes to ions, particularly Na+ and
indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange.

-i- SUBCNIT: Momomer and homotetramer.

-i- SUBCNILULAR LOCATION: Secreted.
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TURN
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PIR; A01762; MEHBCI.
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REVIEW.
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PDB; 1BH1; 06-JAN-99.
InterPro; 1PR002116; Melittin.
Pfam; PF01372; Melittin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Expressed by the venom gland. MISCELLANEOUS: N-formyl-melittin major has 80% of the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE MELLITIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWW="http://www.expasy.org/spotlight/articles/sptlt012.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE: NAME=Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE=Issue 12 of July 2001;
                                                                                                                                                                                                                                                                                                            μ
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD014636; Melittin; 1.
                      precursor.
                                                                                                                                                                                                                                                           MKFLVNVALVFMVVYISYIYA
                                                                                                                                                                                                                                                                                             MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                            45
54
55
7 AA;
                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
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044421
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                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7585
                                                                                                                                                                                                                                                                                                                                                                            10.8%;
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X
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                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.0022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQQG -> KR(
ARTIFACT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   607F52C091C23BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORMYLATION (ABOUT 10% OF THE MOLECULES).
AMIDATION (G-70 PROVIDE AMIDE GROUP).
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                                                                                                                                                                                                                                                             21
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VGLD_HSV1H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashi w.J., Zhang S.F., Zhang C.X., Cheng J.A.;

Toloning and sequencing of cDNA coding for prepromelittin of Polistes are "Cloning and sequencing of cDNA coding for prepromelittin of Polistes are "Cloning and sequencing of cDNA coding for prepromelittin of Polistes are "Cloning and sequencing of cDNA coding for prepromelittin of Polistes are better the property of the SWBL/GenBank/DDBJ databases.

Submitted (FEB-2002) to the SWBL/GenBank/DDBJ databases into cell code in the sequence of the code in the sequence of the code in the sequence of the probably, as a result of its continuous and has multiple effects, probably, as a result of its code interaction with negatively charged phospholipids. It inhibits well known transport pumps such as the Na(+)-K(+)-ATPase and the CC H(+)-K(+)-ATPase. Increases the permeability of cell membranes to ions, particularly Na+ and indirectly Ca(2+), because of the CC ions, particularly Na+ and indirectly Ca(2+), because of the SUBUNIT: Momomer and homotetramer (By similarity).

C-1- SUBCELILLAR LOCATION: Secreted (By similarity).

C-1- SUBCELILLAR LOCATION: Secreted (By similarity).

C-1- SUBCELILLAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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01-JAN-1988
16-OCT-2001
                                                                                                                                                                                                                                                                       VGLD_HSV1H
P06476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vespula maculifrons (Eastern yellow jacket) (Wasp).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vesp
Vespidae; Vespinae; Vespula.
SEQUENCE FROM N.A.

MEDLINE=84131549; PubMed=6321120;

Lasky L.A., Dowbenko D.J.;

"DNA sequence analysis of the type-common glycoprotein-D herpes simplex virus types 1 and 2.";

DNA 3:23-29(1984).
                                                                                                                                  Herpes simplex virus (type 1 / strain Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                     Glycoprotein D precursor. GD OR US6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF487911; AAO12205.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom gland;
Shi W.J., Zhang S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                     NCBI_TaxID=10305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01372; Melittin;
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                             STANDARD;
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43
                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 102; DB 1; 100.0%; Pred. No. 0.0022; ... Mismatches 0;
                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Amidation.
BY SIMILARITY.
REMOVED BY A DIPEPTIDYLPEPTIDASE
SIMILARITY).
MELITTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
607F52C091C23BB6
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                                                                                                                                                     Herpesviridae,
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Query Match
Best Local S
Matches 19
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MEDILINE-85160822; PubMed=2984429;

MCGGeoch D.J., Dolan A., Donald S., Rixon F.J.;

"Sequence determination and genetic content of the short unique region
in the genome of herpes simplex virus type 1.";

J. Mol. Biol. 181:1-13(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _HSV11
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CARBOHYD
CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGLD HSV11 STANDARD; PRT; 3

Q69091; O12544; O12833; P03171;

21-JUL-1986 (Rel. 01, Created)

16-OCT-2001 (Rel. 40, Last sequence up

16-OCT-2001 (Rel. 40, Last annotation

Glycoprotein D precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002896; Herpes_glycop_D.

Pfam; PF01537; Herpes_glycop_D; 1.

Glycoprotein; Transmembrane; Signal.

SIGNAL 1 25 POTENTIAL.

SIGNAL 1 26 393 GLYCOPROTEIN D.

CHAIN 26 393 GLYCOPROTEIN D.
                                                                                                                                                                                                   McGeoch D.J.;
Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                      Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                              GD OR Use.
Herpes simplex virus (type 1 / strain 17).
Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR US6.
                                                                                                                                           MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GB, GC, GG, GD, GI, AND GE.
SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB, GC, GG, GD, GI, AND GE.
SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1:
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145
286
393 AA;
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339
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364
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393
338
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Pred. No.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ARG/LYS-RICH (HIGHLY BASIC; PROBABLY SERVES TO ANCHOR THE GLYCOPROTEIN IN THE MEMBRANE).
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0.032;
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RESULT 7
VGLD_HSV1A
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Best Local S
Matches 19
PIK; A4/52/; A4/52/;
InterPro; IPRO/02896; Herpes_glycop_D: 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

Refam; PF01537; Herpes_glycop_D; 1.

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Refam; PF01537; Herpes_glycop_D; 1.

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Refam; PF01537; Herpe
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SIGNAL
CHAIN 2
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01-JUN-1994
16-OCT-2001
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SEQUENCE
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P36318;
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain Angelotti)
Viruses; dsDNA viruses, no RNA stage; Herpesviri
Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GB, GC, GG, GD, GI, AND GE.
-1- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 izumi K.M., Stevens J.G.;
"Molecular and biological characterization of a herpes simplex virus
type 1 (HSV-1) neuroinvasiveness gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein D
GD OR US6.
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Pfam; PF01537; Herpes_glycop_
Glycoprotein; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type 1 (HSV-1) neuroinvasivene
J. Exp. Med. 172:487-496(1990)
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(Rel. 40, Last and
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

ARG/LYS-RICH (HIGHLY BASIC; PROBABLY SERVES TO ANCHOR THE GLYCOPROTEIN IN THE MEMBRANE).

N-LINKED (GLCNAC. ..) (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson R.J., Weis J.H., Salstrom J.S., Enq
"Herpes simplex virus type-1 glycoprotein
and expression in Escherichia coli.";
Science 218:381-384(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus (type 1 / strain
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein D precursor. GD OR US6.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
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                                                                                SEQUENCE
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SIGNAL
                                                                                                                                                                                                                                                                  PIR; A94268; VGBED1
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Glycoprotein; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GB, GC, GG, GD, GI, AND GE.
SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
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159 QPELAPEDPEDSALLEDPV 177
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                                                                                         CYTOPLASMIC (POTENTIAL)

ARG/LYS-RICH (HIGHLY BASIC; PROBABLY SERVES TO ANCHOR THE GLYCOPROTEIN IN THE MEMBRANE).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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Signal; 3D-structure.
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                                               Score 99;
Pred. No.
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Pred. No.
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                                                DB 1;
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                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES=A.c.cerana, V.magnifica, and V.v.nigrithorax;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apis cerana cerana (Oriental honeybee)
Vespa magnifica (Hornet), and
Vespa velutina nigrithorax (Hornet)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
                                                                                        SEQUENCE
                                                                                                                                                         Cytolysis;
SIGNAL
                                                                                                                                                                                                                            EMBL; AF487907; AAO12201.1; -.
                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Momomer and homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE MELLITIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Hymenoptera;
Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melittin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEL_APICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=94128, 202807,
                                                                                                                                                PROPEP
                                                                                                                                                                                roDom;
                                                                                                                                                                                           Pfam; PF01372; Melittin; 1.
                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                    AF487910; AA012204.1; -. AF487908; AA012202.1; -.
                                                                                                                                            P01372; Melittin; 1.
PD014636; Melittin; 1.
Hs; Hemolysis; Toxin; Signal; Amidation.
BY SIMILARITY.
POYTON BY A DIPE!
                                                     Similarity
             MKFLVNVALVFMVVYISYIYAR----LPDGITKAGEDA 34
MKFLVNVALVEMVVYISFIYAAPEPEPAPEAEAEADAEA
                                         10.4%;
nilarity 59.0%;
Conservative
                                                                                        70
                                                                                                             44
69
                                                                                        <u>Α</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                        7543 MW;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202809;
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annotation updat
                                          4.
                                          Score 98.5; D
Pred. No. 0.00
4; Mismatches
                                                                                     MELITTIN.
AMIDATION (G-70 PROVIDE SIMILARITY).
DA6B17C086C9560C CRC64;
                                                                                                                                  REMOVED BY A DIPEPTIDYLPEPTIDASE SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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  (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AA
                                                     0.0048;
                                                                DB 1;
39
                                                                 Length
                                                                                                                                                                                                                                                                          by and for
                                                                                                              AMIDE GROUP)
                                                                                                                                                                                                                                                                                                restrictions
                                                                 70
                                                                                                                                                                                                                                                                                                          EMBL outstation
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RESULT 10

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Best Local S
Matches 23
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28-FEB-2003
28-FEB-2003
                                                                                                                                                     COPI DROME STANDARD; PRT; 1409 AA. P04146; Q03728; Q24280; Q24555; Q24585; Q24586; 01-NOV-1986 (Rel. 03, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEL_POLHE
P59261;
                                                                                                     Copia protein [Contains: (EC 3.4.23.-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shi W.J., Zhang S.F., Zhang C.X., Cheng J.A.; "Cloning and sequencing of CDN acding for prepromelittin hebraeus, Vespa magnifica and Vespula maculifrons."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polistes hebraeus (Paper wasp).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
Vespidae; Polistinae; Polistes.
  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                   COPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=202806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Has strong hemolytic activity. Integrates into cell membranes and has multiple effects, probably, as a result of its interaction with negatively charged phospholipids. It inhibits well known transport pumps such as the Na(+)-K(+)-ArPase and the H(+)-K(+)-ArPase. Increases the permeability of cell membranes to ions, particularly Na+ and indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By similarity). SUBCULTI. Momomer and homocetramer (By similarity). SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Expressed by the venom gland. SIMILARITY: BELONGS TO THE MELLITIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01372; Melittin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF487909; AAO12203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F01372; Melittin; 1.
PD014636; Melittin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            MKFLVNVALVFMVVYISYIYAR----LPDGITKAGEDA 34
                                                                                                                                                                                                                                                                                                                                                                                               MKFLVNVALVFMVVYISFIYAAPEPEPAPEAEAEADAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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(Rel. 41, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4
69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7513 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin;
                                                                                                                                   Copia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Amidation.

BY SIMILARITY.

REMOVED BY A DIPEPTIDYLPEPTIDASE (BY SIMILARITY).

MELITTIN.

MELITTIN.

ANIDATION (G-70 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA70167086C9560C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 70;
                                                                                                                                   Copia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                      Q24587;
                                                                                                                                protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Polistes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ت</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for commerc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
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R InterPro; lrave; 1.

R InterPro; lrave; 1.

Pfam; pf00665; rve; 1.

DR Pfam; pf00098; zf-CCHC; 1.

DR PRINTS; pf00099; c2HCZNFINGER.

DR PRONTIS; SM00343; ZnF CCHC; 1.

DR PROSITE; p500141; ASP PROTEASE; FALSE NEG.

DR PROSITE; p550158; ZF CCHC; 1.

Transposable element; Hydrolase; Aspartyl protease; ATP-binding; KW Polyprotein; Alternative splicing; Polymorphism; Zinc-finger.

KW Polyprotein; Alternative splicing; Dolfmorphism; Zinc-finger.

CHAIN 271 1409 COPIA VLP PROTEIN (POTENTIAL).

COPIA PROTEASE (POTENTIAL).

COPIA PROTEASE (POTENTIAL).
                                                      EMBL; X04456; CAA28054.2; -. EMBL; X02599; CAA26444.1; -. EMBL; X02599; CAA26445.1; -. EMBL; X02600; CAA26447.1; -. EMBL; X02600; CAA26447.1; -. EMBL; X13719; CAA31997.1; -. EMBL; X54147. CAA38086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autocatalytic processing.";
EMBO J. 9:535-541(1990)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emori Y., Shiba T., Kanaya
"The nucleotide sequences
virus-like particles.";
Nature 315:773-776(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                     FlyBase; FBgn0013437; copia\GIP.
InterPro; IPR001969; Aspprotease_site.
InterPro; IPR001584; Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller K., Rosenbaum J., Zbrzezna V., I
"The nucleotide sequence of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete nucleotide sequence of the Drosophila transposable element copia: homology between copia and retroviral proteins."; Mol. Cell. Biol. 5:1630-1638(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM LONG)
MEDLINE=85267679; PubMed=2410772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Virus-like particle formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshioka K., Honma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The nucleotic
2.1-kb mRNA.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85240569; PubMed=2409449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mount S.M., Rubin
                                                                                                                                                                                                                                                                                    MEROPS; A11.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90151630; PubMed=1689241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:2134-2134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=89183629; PubMed=2538806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EV
                                                                                                                                                                                                                                                                                                    A03324; OFFFCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P04146-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORM SHORT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanaya S., Inouye suences of copia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE BELONGS TO PEPTIDASE FAMILY All.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2-10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHORT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M., Kondo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Drosophila copia through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inouye S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     005226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pogo A.O.;
a melanogaster copia-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S., Yuki S., Saigo K.; copia-related RNA in
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VGLD HSV2
VGLD HSV2
ID VGLD HSV2
STANDARD; PRT; 393 AA.
AC P03172;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein D precursor.
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the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                STRAIN=BBKC;

Terhune S.S., Coleman K.T., Sekulovich R., Burke R.L., Spear P.G.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND

2: GH, GB, GC, GG, GI, AND GE.

-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lasky L.A., Dowbenko D.J.;
"DNA sequence analysis of the type-common glycoprotein-D genes herpes simplex virus types 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of the Herpes simplex virus type 2 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=84159516; PubMed=6323270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a cept the Swiss Institute of Bioinformatics and the EMBL
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STTGYLFKMFDFWLICWNTKRONS -> VQQGIYSKCLILI
SFVGIQRDRTQ (IN VARIANT COPIA-RELATED).

MISSING (IN VARIANT COPIA-RELATED).

D->A: LOSS OF ACTIVITY.

S -> N (IN REF. 2; CAA26447).

I -> V (IN REF. 2; CAA26447).

Q -> E (IN REF. 2; CAA26447).
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L outstation -
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZYGRO
REP1 ZYGRO
P13778;
01-JAN-1990
                      PIR; S28:
Plasmid;
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CARBOHYD
                                                                  EMBL; X02398; CAA26244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          Muta T., Oshima
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85210904; PubMed=3889347;
Araki H., Jearnpipatkul A., Tatsumi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
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Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                       "Molecular and functional organization of yeast plasmid pSR1.";

J. Mol. Biol. 182:191-203(1985).

I-FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
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                                                S28354; S28354.
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17; Conserv
  Trans-acting factor.
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1537; Herpes_glycop_D; 1.
ein; Transmembrane; Signal.
ein; Transmembrane; Signal.
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Last annotation updat
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Pred. No. 0.19;
0; Mismatches
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N-LINKED (GLCNAC. . .)
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A -> S (IN STRAINS 333 AND BBKC).
RSV -> AQM (IN STRAINS 333 AND BB
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    C9B28C381331F018 CRC64
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(POTENTIAL).
(POTENTIAL).
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Query Match

Score 81;

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RESULT 14
CDGT_BACS2
ID CDGT_B
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Schmid G., Englbrecht A., Schmid D.;

"Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase gene from the alkalophilic Bacillus 1-1.";

(In) Huber O., Szejtli J. (eds.);

Proceedings of the fourth international symposium on cyclodextrins, pp.71-76, Kluwer Academic Publishers, Dordrecht and Boston (1988).

-1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.

-1- COFACTOR: BINDS TWO CALCIUM IONS.

-1- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993
01-JUL-1993
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JBC-1998 (Rel. 37, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor
PRINTS; PRO0110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
                                                                                                                                           InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006044; CBD 4.
InterPro; IPR006046; GlyCo_hydro_13.
                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus sp. (strain 1-1).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                InterPro; IPR002909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=29334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclodextrin-glycosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                        am; PF00128; CBM 20; 1.

""; PP0183; TIG; 1.

""; PF0183; TIG; 1.

""; PR00110.
                                                                                                                                                                                                                                                                      MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARTDE RODUCED.
MALTOOLIGOSACCHARTDE RODUCED.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                        KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACS2
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9; Mismatches
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a coptween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YJHT_ECOLI
P39371;
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                     InterPro; IPR006652; Kelch_rep.

Pfam; PF01344; Kelch; 2.

Hypothetical protein; Kelch repeat; Repeat; Signal; Complete SIGNAL

1 POTENTIAL.
                                                               EMBL; U14003; AAA97206.1; ALT_INIT.
EMBL; AE000501; AAC77266.1; ALT_INIT.
EcoGene; EG12562; YjhT.
Enterpro; IFR006652; Kelch_rep.
                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 7 Kelch repeats
                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 23:2105-2119(1995)
                                                                                                                                                                                                                                                                                                                       "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes.";
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sc
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                         Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
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YJHT OR B4310.
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
protein yjhT precursor.
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Pred. No. 4.5;
28; Mismatches
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        HYPOTHETICAL PROTEIN YJHT.
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Search complete	252 -	159 (201)	108 \	148 (68 -	88	18 1	Query Match Best Local Si Matches 36;	SEQUENCE	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	
Search completed: January 22, 2004, 11:39:41	152KLAPVSSPD 260	159 QPELAPEDPED 169	201 YAGESPWYGTAGAAVVNKGDKTWLINGEAKPGLRTDAVFELDFTGNNLKWN	LO8 VRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDYTSSAYMWNMQYGMVG	48 QNIFNGYFEDLNEAGKDSTAIDKINAHYFDKKAEDYFFNKFLLSFDP-STQQWS	68VGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWN	88 YVFGGIGKNSEGLTQVFNDVHKYNPKTNSWVKLMSHAPMGMAGHVTFVHNGKAYVTGGVN	18 YIYARLPDGITKAGEDALRPWKSTAKHPWPQIEDNRCYIDNGKLFARGSI-	Query Match 8.3%; Score 78.5; DB 1; Length 368; Best Local Similarity 18.8%; Pred. No. 3; Matches 36; Conservative 29; Mismatches 69; Indels 57; Gaps	368 AA; 39572 MW;	338 367 KELCH	287 336 KELCH	222 265 KELCH	174 219	139 173 KELCH	86 137 KELCH	7 40 84 KELCH 1.	
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